

10-524

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ACCESS DB #

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Scientific and Technical Information Center

SEARCH REQUEST FORM

CRFE

Requester's Full Name: JANE ZARA Examiner #: 77512 Date: 10-12
Art Unit: 1635 Phone Number: 2-0765 Serial Number: 10/604,728
Location (Bldg/Room#): 6033 Mailbox #: 2C18 Results Format Preferred (circle): PAPER DIS

2459

To ensure an efficient and quality search, please attach a copy of the cover sheet, claims, and abstract or fill out the following:

Title of Invention: BIOINFORMATICAALLY DETECTABLE

Inventors (please provide full names): BENTWICH

Earliest Priority Date: 8-13-03

Search Topic:

Please provide a detailed statement of the search topic, and describe as specifically as possible the subject matter elected species or structures, keywords, synonyms, acronyms, and registry numbers, and combine with the concept. Define any terms that may have a special meaning. Give examples or relevant citations, authors, etc., if known.

For Sequence Searches Only Please include all pertinent information (parent, child, divisional, or issued patent number, appropriate serial number.

Please Search Seq ID No: 8797
Please limit to 120 NTS.

Please Search Seq ID No:
5135, 6033, 5136 + 60:

size limit @ to 30 NTS

5135-79na

6033-85na

5136-24na

6034-24na
CB

www.science.gov

10/16/06
eng
tool
10/16/06
Korphen
C411

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GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 16, 2006, 13:57:30 ; Search time 590.797 Seconds
(without alignments)
2597.742 Million cell updates/sec

Title: US-10-604-726A-6034
Perfect score: 24
Sequence: 1 ugagagggcgguaagcgucc 24

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 6366136 seqs, 31973710525 residues

Total number of hits satisfying chosen parameters: 1796954

Minimum DB seq length: 0
Maximum DB seq length: 30

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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3: gb_ph.*
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5: gb_pr.*
6: gb_ro.*
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9: gb_un.*
10: gb_vi.*
11: gb_ov.*
12: gb_htg.*
13: gb_in.*
14: gb_om.*
15: gb_ba.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	15.8	65.8	24	2	AX443910 Sequence
2	15.8	65.8	25	2	AX447886 Sequence
3	14.6	60.8	24	2	AX538707 Sequence
4	13.8	57.5	22	2	AR036420 Sequence
5	13.8	57.5	22	2	I29861 Sequence
6	13.4	55.8	28	2	BD141786 Novel G p
7	13.4	55.8	28	2	BD173668 Novel phy
8	13.4	55.8	28	2	BD181737 Novel G p
9	13.2	55.0	25	2	AR148541 Sequence
10	13.2	55.0	25	2	I62320 Sequence
11	13	54.2	17	2	AX215297 Sequence
12	13	54.2	17	2	AX215298 Sequence
13	13	54.2	17	2	AX215299 Sequence
14	13	54.2	17	2	AX215300 Sequence
15	13	54.2	20	2	AX298773 Sequence
16	13	54.2	27	2	AX347840 Sequence
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21	12.6	52.5	19	2	AR628705	Sequence
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23	12.6	52.5	20	2	AR150043	Sequence
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25	12.6	52.5	20	2	AR442443	Sequence
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32	12.6	52.5	28	2	AR534679	Sequence
33	12.6	52.5	28	2	AX004269	Sequence
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37	12.6	52.5	30	2	AR167568	Sequence
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ALIGNMENTS

RESULT 1
AX443910
LOCUS AX443910 24 bp DNA linear PAT 03-JUL-2002
DEFINITION Sequence 365 from Patent WO0216649.
ACCESSION AX443910
VERSION AX443910.1 GI:21691188
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1
AUTHORS Gunderson, K.
TITLE Probes and decoder oligonucleotides
JOURNAL Patent: WO 0216649-A 365 28-FEB-2002;
Illumina, Inc. (US)
FEATURES
Location/Qualifiers
source
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/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Computer Generated Probe Sequence."

ORIGIN

Query Match 65.8%; Score 15.8; DB 2; Length 24;
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Matches 14; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
QY 2 GAGAGGGCGGUAAGGC 20
DB 4 GAGAGCGGTGTTAAGC 22
RESULT 2
AX447886
LOCUS AX447886 25 bp DNA linear PAT 03-JUL-2002
DEFINITION Sequence 4341 from Patent WO0216649.
ACCESSION AX447886
VERSION AX447886.1 GI:21696785
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM

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CC nucleic acid sequence by attaching a adapter nucleic acid (ABQ00010-
CC ABQ13409) to a target nucleic acid to form a modified target nucleic acid
CC and contacting the modified target nucleic acid with (1). The steps of
CC above method is useful for detecting a target nucleic acid, which further
CC comprises detecting the presence of the modified target nucleic acid
XX
XX
SQ Sequence 24 BP; 7 A; 2 C; 10 G; 5 T; 0 U; 0 Other;

Query Match 18.6%; Score 15.8; DB 6; Length 24;
Best Local Similarity 73.7%; Pred. No. 5.9e+04;
Matches 14; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 16 GAGAGGGCGUGUUAAGGC 34
||||| | : : : : :
Db 4 GAGAGGGCGTGTGTTAAGGC 22

RESULT 11
ABQ11043/c
ID ABQ11043 standard; DNA; 24 BP.
AC
XX
AC ABQ11043;
XX
DT 11-JUN-2002 (first entry)
XX
XX Oligonucleotide adapter/capture probe 11034.
DE
XX
KW Oligonucleotide array; adapter sequence; probe; ss.
XX
OS Synthetic.
XX
XX WO200216649-A2.
XX
XX 28-FEB-2002.
XX

PF 27-AUG-2001; 2001WO-US026519.
XX
XX 25-AUG-2000; 2000US-0227948P.
PR
XX 29-AUG-2000; 2000US-0228854P.
XX
XX (ILLU-) ILLUMINA INC.
PA
XX
XX Gunderson K;
PI
XX
XX WPI; 2002-292068/33.
DR

PT Array comprising adapter sequences useful for immobilizing or detecting a
PT target nucleic acid sequence, has different addresses comprising
PT different specific capture probes.
XX
XX Claim 1; Page 225; 261pp; English.
XX
XX The invention relates to an oligonucleotide array (1) comprising at least
CC 25 different addresses (adapter sequences) with each comprising a
CC different capture probe selected from a group consisting of the sequences
CC given in ABQ00010-ABQ13409. (1) is useful for immobilizing a target
CC nucleic acid sequence by attaching a adapter nucleic acid (ABQ00010-
CC ABQ13409) to a target nucleic acid to form a modified target nucleic acid
CC and contacting the modified target nucleic acid with (1). The steps of
CC above method is useful for detecting a target nucleic acid, which further
CC comprises detecting the presence of the modified target nucleic acid
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XX Sequence 24 BP; 5 A; 10 C; 2 G; 7 T; 0 U; 0 Other;

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Best Local Similarity 73.7%; Pred. No. 5.9e+04;
Matches 14; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

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ID ABQ12538 standard; DNA; 25 BP.
XX
XX AC ABQ12538;
XX
XX DT 11-JUN-2002 (first entry)
XX
XX DE Oligonucleotide adapter/capture probe 12529.
XX
XX KW Oligonucleotide array; adapter sequence; probe; ss.
XX
XX OS Synthetic.
XX
XX PN WO200216649-A2.
XX
XX 28-FEB-2002.
XX

PF 27-AUG-2001; 2001WO-US026519.
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XX 25-AUG-2000; 2000US-0227948P.
PR
XX 29-AUG-2000; 2000US-0228854P.
XX
XX (ILLU-) ILLUMINA INC.
PA
XX
XX Gunderson K;
PI
XX
XX WPI; 2002-292068/33.
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PT Array comprising adapter sequences useful for immobilizing or detecting a
PT target nucleic acid sequence, has different addresses comprising
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CC nucleic acid sequence by attaching a adapter nucleic acid (ABQ00010-
CC ABQ13409) to a target nucleic acid to form a modified target nucleic acid
CC and contacting the modified target nucleic acid with (1). The steps of
CC above method is useful for detecting a target nucleic acid, which further
CC comprises detecting the presence of the modified target nucleic acid
XX
XX Sequence 25 BP; 7 A; 2 C; 10 G; 6 T; 0 U; 0 Other;

Query Match 18.6%; Score 15.8; DB 6; Length 25;
Best Local Similarity 73.7%; Pred. No. 6e+04;
Matches 14; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 16 GAGAGGGCGUGUUAAGGC 34
||||| | : : : : :
Db 5 GAGAGGGCGTGTGTTAAGGC 23

RESULT 13
ABQ12579/c
ID ABQ12579 standard; DNA; 25 BP.
XX
XX AC ABQ12579;
XX
XX DT 11-JUN-2002 (first entry)
XX
XX DE Oligonucleotide adapter/capture probe 12570.
XX
XX KW Oligonucleotide array; adapter sequence; probe; ss.
XX
XX OS Synthetic.
XX
XX PN WO200216649-A2.
XX
XX 28-FEB-2002.
XX

PF 27-AUG-2001; 2001WO-US026519.
XX
XX 25-AUG-2000; 2000US-0227948P.
PR
XX 29-AUG-2000; 2000US-0228854P.
XX
XX (ILLU-) ILLUMINA INC.
PA
XX
XX Gunderson K;
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XX WPI; 2002-292068/33.
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CC nucleic acid sequence by attaching a adapter nucleic acid (ABQ00010-
CC ABQ13409) to a target nucleic acid to form a modified target nucleic acid
CC and contacting the modified target nucleic acid with (1). The steps of
CC above method is useful for detecting a target nucleic acid, which further
CC comprises detecting the presence of the modified target nucleic acid
XX
XX Sequence 25 BP; 7 A; 2 C; 10 G; 6 T; 0 U; 0 Other;

Query Match 18.6%; Score 15.8; DB 6; Length 25;
Best Local Similarity 73.7%; Pred. No. 6e+04;
Matches 14; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 16 GAGAGGGCGUGUUAAGGC 34
||||| | : : : : :
Db 5 GAGAGGGCGTGTGTTAAGGC 23

RESULT 13
ABQ12579/c
ID ABQ12579 standard; DNA; 25 BP.
XX
XX AC ABQ12579;
XX
XX DT 11-JUN-2002 (first entry)
XX
XX DE Oligonucleotide adapter/capture probe 12570.
XX
XX KW Oligonucleotide array; adapter sequence; probe; ss.
XX
XX OS Synthetic.
XX
XX PN WO200216649-A2.
XX
XX 28-FEB-2002.
XX

PF 27-AUG-2001; 2001WO-US026519.
XX
XX 25-AUG-2000; 2000US-0227948P.
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XX 29-AUG-2000; 2000US-0228854P.
XX
XX (ILLU-) ILLUMINA INC.
PA
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XX Gunderson K;
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XX WPI; 2002-292068/33.
DR

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CC different capture probe selected from a group consisting of the sequences
CC given in ABQ00010-ABQ13409. (1) is useful for immobilizing a target
CC nucleic acid sequence by attaching a adapter nucleic acid (ABQ00010-
CC ABQ13409) to a target nucleic acid to form a modified target nucleic acid
CC and contacting the modified target nucleic acid with (1). The steps of
CC above method is useful for detecting a target nucleic acid, which further
CC comprises detecting the presence of the modified target nucleic acid
XX
XX Sequence 25 BP; 7 A; 2 C; 10 G; 6 T; 0 U; 0 Other;

Query Match 18.6%; Score 15.8; DB 6; Length 25;
Best Local Similarity 73.7%; Pred. No. 6e+04;
Matches 14; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 16 GAGAGGGCGUGUUAAGGC 34
||||| | : : : : :
Db 5 GAGAGGGCGTGTGTTAAGGC 23

RESULT 13
ABQ12579/c
ID ABQ12579 standard; DNA; 25 BP.
XX
XX AC ABQ12579;
XX
XX DT 11-JUN-2002 (first entry)
XX
XX DE Oligonucleotide adapter/capture probe 12570.
XX
XX KW Oligonucleotide array; adapter sequence; probe; ss.
XX
XX OS Synthetic.
XX
XX PN WO200216649-A2.
XX
XX 28-FEB-2002.
XX

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GenCore version 5.1.9

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Run on: October 16, 2006, 14:22:20 ; Search time 1299 Seconds
(without alignments)

3889.027 Million cell updates/sec

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Perfect score: 79

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Total number of hits satisfying chosen parameters: 2740178

Minimum DB seq length: 0

Maximum DB seq length: 100

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	20.2	25.6	49	2	AX772410	Sequence
3	20	25.3	93	2	AX987628	Sequence
4	20	25.3	93	2	BD122487	EST and e
5	20	25.3	93	2	AR426934	Sequence
6	19.8	25.1	63	2	E08253	linker. 9/1
7	19.8	25.1	92	14	AY753640	Sus scrofa
8	19.4	24.6	97	2	AR165723	Sequence
9	19.4	24.6	97	2	AR304919	Sequence
10	19.2	24.3	51	2	BD034273	Sequence
11	19.2	24.3	51	2	AR734534	Sequence
12	19.2	24.3	51	2	AX898740	Sequence
13	19.2	24.3	100	6	RNU12530	Sequence
14	19	24.1	65	2	E08252	linker. 9/1
15	19	24.1	65	2	AX184576	Sequence
16	19	24.1	85	7	BX294351	Arabidops
17	18.8	23.8	39	2	A86879	Sequence 19
18	18.8	23.8	39	2	BD070385	Factor X-

19	18.8	23.8	39	2	AR340859	Sequence
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21	18.8	23.8	72	2	CS254876	Sequence
22	18.8	23.8	79	2	AR126073	Sequence
23	18.8	23.8	81	10	AF473711	Hepatitis
24	18.6	23.5	55	2	BD270121	Method of
25	18.6	23.5	65	2	CQ534358	Sequence
26	18.6	23.5	69	6	MMTRB138	Mouse mRNA
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28	18.6	23.5	94	2	CQ080813	Sequence
29	18.6	23.5	94	2	CQ115279	Sequence
30	18.6	23.5	94	2	CQ154107	Sequence
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ALIGNMENTS

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ACCESSION	AX184498.1	GI:15135853				
VERSION						
KEYWORDS						
SOURCE	Homo sapiens (human)					
ORGANISM	Homo sapiens					
REFERENCE	1	Schlegel, R., Deeds, J., Berger, A. and Zhao, X.				
AUTHORS		Genes, compositions, kits, and methods for identification,				
TITLE		assessment, prevention, and therapy of cervical cancer				
JOURNAL		Patent: WO 0142467-A 193 14-JUN-2001;				
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QY	76	CUCC	79			
Db	66	CGCC	69			
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LOCUS						

DEFINITION					
Sequence 200 from Patent WO03042407.					
ACCESSION					
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VERSION					
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KEYWORDS					
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SOURCE					
Drosophila melanogaster					
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.					
REFERENCE					
1 Dickson,B., Berger,J., Suzuki,T. and Knoblich,J. Method for identifying therapeutic targets by use of genetic screens in drosophila melanogaster Patent: WO 03042407-A 200 22-MAY-2003; BOEHRINGER INGELHEIM INTERNATIONAL GMBH; CD Patents (DE) FEATURES					
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Dd					
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LOCUS					
AX987628 93 bp DNA linear PAT 15-JAN-2004					
DEFINITION					
Sequence 18431 from Patent EP1104808.					
ACCESSION					
AX987628					
VERSION					
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KEYWORDS					
Homo sapiens (human)					
SOURCE					
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominiidae; Homo.					
REFERENCE					
1 Dumas Milne Edwards,J.B., Jobert,S. and Giordano,J.Y. ESTs and encoded human proteins Patent: EP 1104808-A 18431 06-JUN-2001; JOURNAL					
Genet (FR)					
FEATURES					
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/mol_type="unassigned DNA"					
/db_xref="taxon:9606"					
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Qy					
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Dd					
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LOCUS					
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EST and encoded human protein.					
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BD122487.1 GI:23217432					
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JP 200201789-A/14564.					
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Homo sapiens (human)					
ORGANISM					
Homo sapiens					

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominiidae; Homo. 1 (bases 1 to 93) Edwards,J.B.D.M., Jobert,S. and Giordano,J.E. EST and encoded human protein Patent: JP 2002010789-A 14564 15-JAN-2002; GENSET CORP	
COMMENT	
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PC C12N15/09,C12N15/09,C07K14/47,C07K16/18,C12N1/15,C12N1/19, PC C12N1/21,	
PC C12N5/10,C12P21/02,C12P21/08,C12Q1/68,C12N15/00,C12N5/00, PC C12N15/00	
CC n=a, g, c or t Location/Qualifiers	
FH Key	
FT misc_feature 63..64	
FT misc_feature 83.	
FEATURES	
source	
Location/Qualifiers	
1..93	
/organism="Homo sapiens"	
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Best Local Similarity 63.9%; Pred.No.3e+04;	
Matches 23; Conservative 3; Mismatches 10; Indels 0; Gaps 0;	
Qy 5 GGCGGGGAGACGACGGCGUCUGGCCCUAAU 40	
Dd 58 GGCGGGCGGCAGCACGGCTCAGGCCCTGCAGT 23	
RESULT 5	
AR426934/c	
LOCUS AR426934 93 bp DNA linear PAT 18-DEC-2003	
DEFINITION Sequence 18431 from patent US 6639063.	
ACCESSION AR426934	
VERSION AR426934.1 GI:40182044	
KEYWORDS .	
SOURCE Unknown.	
ORGANISM Unclassified.	
REFERENCE	
AUTHORS 1 (bases 1 to 93)	
TITLE Edwards,J.-B.D.M., Jobert,S. and Giordano,J.-Y.	
JOURNAL EST's and encoded human proteins	
Patent: US 6639063-A 18431 28-OCT-2003;	
Genset S.A.;;	
WOX;	
FEATURES	
source	
Location/Qualifiers	
1..93	
/organism="unknown"	
/mol_type="genomic DNA"	
ORIGIN	
Query Match 25.3%; Score 20; DB 2; Length 93;	
Best Local Similarity 63.9%; Pred.No.3e+04;	
Matches 23; Conservative 3; Mismatches 10; Indels 0; Gaps 0;	
Qy 5 GGCGGGGAGACGACGGCGUCUGGCCCUAAU 40	
Dd 58 GGCGGGCGGCAGCACGGCTCAGGCCCTGCAGT 23	
RESULT 6	
E08253/c	
LOCUS E08253 63 bp DNA linear PAT 29-SEP-1997	

DEFINITION	linker.
ACCESSION	E08253
VERSION	E08253.1 GI:2176374
KEYWORDS	JP 1994279497-A/12.
SOURCE	unidentified
ORGANISM	unclassified sequences.
REFERENCE	1 (bases 1 to 63)
AUTHORS	Doi,T., Iwasaki,A., Saino,S., Kimura,S. and Oguchi,M.
TITLE	THROMBIN-BINDING SUBSTANCE AND ITS PRODUCTION
JOURNAL	Patent: JP 1994279497-A 12 04-OCT-1994;
COMMENT	KOWA CO
OS	None
OC	Artificial sequences.
PN	JP 1994279497-A/12
PD	04-OCT-1994
PE	25-NOV-1991 JP 1991308976
PR	30-NOV-1990 JP 90P 335720, 25-FEB-1991 JP 91P 30271 PI
DOI	TAKEISHI, IWASAKI AKIO, SAINO SUKEYUKI, KIMURA SHIGERU, PI
OGUCHI MASAO	
PC	C07K13/00, A61K37/02, C12N1/21, C12N5/10, C12N15/12, C12N15/70, PC
C12P21/02.	
PC	(C12N1/21, C12R1:19), (C12P21/02, C12R1:91) ;
CC	strandedness: Single;
CC	topology: Linear;
FH	Key Location/Qualifiers
FT	source 1..63
FT	/organism='Artificial sequences'.
FEATURES	source Location/Qualifiers
source	1..63
	/organism="unidentified"
	/mol_type="genomic DNA"
	/db_xref="taxon:32644"
ORIGIN	
Query Match	25.1%; Score 19.8; DB 2; Length 63;
Best Local Similarity	59.0%; Pred. No. 3.4e+04;
Matches	23; Conservative 4; Mismatches 12; Indels 0; Gaps 0;
QY	3 AGGGCGGGGAGACGACGCGCGCUCUGGCCCUUAUUG 41
DB	40 AGGTGACGACGACGACGCGCTGTGGCGACTGACTCG 2
RESULT 7	
AY753640S2/c	
LOCUS	AY753640S2 92 bp DNA linear MAM 20-OCT-2004
DEFINITION	Sus scrofa cAMP response element binding protein (CREB) gene, exon 4 and partial cds.
ACCESSION	AY753641
VERSION	AY753641.1 GI:54125959
KEYWORDS	
SEGMENT	2 of 7
SOURCE	Sus scrofa (pig)
ORGANISM	Sus scrofa
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae; Sus.
REFERENCE	1 (bases 1 to 92)
AUTHORS	Chmurzynska,A. and Switonski,M.
TITLE	Direct Submission
JOURNAL	Submitted (20-SEP-2004) Department of Animal Genetics and Breeding, Agricultural University of Poznan, Wolynska 33, Poznan 60-637, Poland
FEATURES	Location/Qualifiers
source	1..92
	/organism="Sus scrofa"
	/mol_type="genomic DNA"
	/db_xref="taxon:9823"
mRNA	<1..>92
	/gene="CREB"
	/product="cAMP response element binding protein"
CDS	
<1..>92	
/gene="CREB"	
/codon_start=1	
/product="cAMP response element binding protein"	
/protein_id="AAV30667.1"	
/db_xref="GI:54125966"	
/translation="APTITVLVQLPNGQTQVGHVIGIAQPSVIQS"	
<1..>92	
/gene="CREB"	
/number=4	
exon	
ORIGIN	
Query Match	25.1%; Score 19.8; DB 14; Length 92;
Best Local Similarity	41.8%; Pred. No. 3.6e+04;
Matches	23; Conservative 10; Mismatches 22; Indels 0; Gaps 0;
QY	23 GGCUCUGGCCCUUAUUGUACUUGCGGCGUGUAUGUCUCUUCUUGCGCACU 77
DB	77 GCGTCGGCGCGCTGAATAACTCCATGACTTGAACCTGTCTGCCCATTTGGCAGCT 23
RESULT 8	
AR165723/c	
LOCUS	AR165723 97 bp DNA linear PAT 17-OCT-2001
DEFINITION	Sequence 288 from patent US 6280932.
ACCESSION	AR165723
VERSION	AR165723.1 GI:16240708
KEYWORDS	
SOURCE	Unknown.
ORGANISM	Unknown.
REFERENCE	1 (bases 1 to 97)
AUTHORS	Parma,D.H., Hicke,B., Bridonneau,P. and Gold,L.
TITLE	High affinity nucleic acid ligands to lectins
JOURNAL	Patent: US 6280932-A 288 28-AUG-2001;
FEATURES	Location/Qualifiers
source	1..97
	/organism="unknown"
	/mol_type="unassigned DNA"
ORIGIN	
Query Match	24.6%; Score 19.4; DB 2; Length 97;
Best Local Similarity	31.1%; Pred. No. 5.1e+04;
Matches	19; Conservative 16; Mismatches 26; Indels 0; Gaps 0;
QY	19 GAGCGGCGUCGCGCCCUUAUUGUACUUGCGGCGUGUAUGUCUUCUUGCGCACCU 78
DB	90 GTGACCTCTCTGTGAACTTACTTCTGCTTTGTTTCTTCTTCTTCTTCTTCTTCTT 31
QY	79 C 79
DB	30 C 30
RESULT 9	
AR304919/c	
LOCUS	AR304919 97 bp RNA linear PAT 12-JUN-2003
DEFINITION	Sequence 288 from patent US 6544959.
ACCESSION	AR304919
VERSION	AR304919.1 GI:31694107
KEYWORDS	
SOURCE	Unknown.
ORGANISM	Unknown.
REFERENCE	1 (bases 1 to 97)
AUTHORS	Parma,D.H., Hicke,B., Bridonneau,P. and Gold,L.
TITLE	High affinity nucleic acid ligands to lectins
JOURNAL	Patent: US 6544959-A 288 08-APR-2003;
FEATURES	Location/Qualifiers
source	1..97
	/organism="unknown"
	/mol_type="unassigned RNA"

[illegible]

JOURNAL Submitted (21-JUL-1994) Cheryl F. Rosen, Medicine, University of Toronto, 100 College Street, Room 317, Toronto, Ontario, M5G 1L5, Canada

FEATURES source
 1. .100 Location/Qualifiers
 /organism="Rattus norvegicus"
 /mol_type="mRNA"
 /strain="Sprague-Dawley"
 /db_xref="taxon:10116"
 /clone="UV126T7"
 /cell_type="keratinocyte"
 /dev_stage="newborn"
 1. .100
 /gene="UV126"
 <1. .>100
 /gene="UV126"

ORIGIN
 Query Match 24.3%; Score 19.2; DB 6; Length 100;
 Best Local Similarity 47.5%; Pred. No. 6e+04;
 Matches 19; Conservative 8; Mismatches 13; Indels 0; Gaps 0;

Qy 40 UGUACUUGCGGCGUAGUUGUCUCCUUCGCCACCUCC 79
 Db 52 TCTATGGCGACTGTTACGTCGCTCCCTCCGCCCCCTCC 91

RESULT 14
 E08252 LOCUS 65 bp DNA linear PAT 29-SEP-1997
 DEFINITION linker.
 ACCESSION E08252
 VERSION E08252.1 GI:2176373
 KEYWORDS JP 1994279497-A/11.
 SOURCE unidentified
 . ORGANISM unclassified sequences.
 REFERENCE 1 (bases 1 to 65)
 AUTHORS Doi, T., Iwasaki, A., Saino, S., Kimura, S. and Oguchi, M.
 TITLE THROMBIN-BINDING SUBSTANCE AND ITS PRODUCTION
 JOURNAL Patent: JP 1994279497-A 11 04-OCT-1994;
 KOWA CO
 OS None
 OC Artificial sequences.
 PN JP 1994279497-A/11
 PD 04-OCT-1994
 PF 25-NOV-1991 JP 1991308976
 PR 30-NOV-1990 JP 90P 335720, 25-FEB-1991 JP 91P 30271 PI
 DOI TAKESHI, IWASAKI AKIO, SAINO SUKEYUKI, KIMURA SHIGERU, PI
 OGUCHI MASAO
 PC C07K13/00, A61K37/02, C12N1/21, C12N5/10, C12N15/12, C12N15/70, PC
 C12P21/02, C12P21/19, C12P21/02, C12R1:91;
 CC (C12N1/21, C12R1:19), (C12P21/02, C12R1:91);
 CC strandedness: Single;
 CC topology: Linear;
 FH Key Location/Qualifiers
 FT source 1. .65
 FT /organism='Artificial sequences'.
 FT Location/Qualifiers
 1. .65
 /organism="unidentified"
 /mol_type="genomic DNA"
 /db_xref="taxon:32644"

FEATURES source
 1. .65 Location/Qualifiers
 /organism="unidentified"
 /mol_type="genomic DNA"
 /db_xref="taxon:32644"

ORIGIN
 Query Match 24.1%; Score 19; DB 2; Length 65;
 Best Local Similarity 62.9%; Pred. No. 6.7e+04;
 Matches 22; Conservative 3; Mismatches 10; Indels 0; Gaps 0;

Qy 3 AGGGCGGGGAGACGACGCGGCGUCUGGCCCUUA 37
 Db 30 AGGTCGACGACGAGCGCGGCTCTGCGACTGA 64

JOURNAL Submitted (06-AUG-2001) linear PAT 06-AUG-2001

AX184576/c AX184576 65 bp DNA linear PAT 06-AUG-2001

LOCUS AX184576 Sequence 271 from Patent WO0142467.

DEFINITION AX184576

ACCESSION AX184576

VERSION AX184576.1 GI:15135934

KEYWORDS Homo sapiens (human)

SOURCE Homo sapiens

ORGANISM Homo sapiens

REFERENCE 1 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.

AUTHORS Schlegel, R., Deeds, J., Berger, A. and Zhao, X.

TITLE Genes, compositions, kits, and methods for identification, assessment, prevention, and therapy of cervical cancer

JOURNAL Patent: WO 0142467-A 271 14-JUN-2001; Millennium Predictive Medicine, Inc. (US)

FEATURES Location/Qualifiers
 1. .65
 /organism="Homo sapiens"
 /mol_type="unassigned DNA"
 /db_xref="taxon:9606"

ORIGIN
 Query Match 24.1%; Score 19; DB 2; Length 65;
 Best Local Similarity 37.5%; Pred. No. 6.7e+04;
 Matches 15; Conservative 10; Mismatches 15; Indels 0; Gaps 0;

Qy 40 UGUACUUGCGGCGUAGUUGUCUCCUUCGCCACCUCC 79
 Db 44 TTTTCTTCGTCNTCGAANANTCTCTCTCCTCGCTNCGCC 5

Search completed: October 16, 2006, 14:44:12
 Job time : 1301 secs

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GenCore version 5.1.1.9
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OM nucleic - nucleic search, using sw model

Run on: October 16, 2006, 14:22:19 ; Search time 302 Seconds
(without alignments)
1823.866 Million cell updates/sec

Title: US-10-604-726A-5135
Perfect score: 79
Sequence: 1 ggagggcggggagagacga.....ucucuccuugccaccucc 79
Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 5244920 seqs, 3486124231 residues 5647924
Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 100

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_8.*
1: Geneseqn1980s.*
2: Geneseqn1990s.*
3: Geneseqn2000s.*
4: Geneseqn2001as.*
5: Geneseqn2001bs.*
6: Geneseqn2002as.*
7: Geneseqn2002bs.*
8: Geneseqn2003as.*
9: Geneseqn2003bs.*
10: Geneseqn2003cs.*
11: Geneseqn2003ds.*
12: Geneseqn2004as.*
13: Geneseqn2004bs.*
14: Geneseqn2005s.*
15: Geneseqn2006s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	23.6	29.9	97	4	Aah68919 Human cer
2	23	29.1	87	6	Ab175509 Corn tass
3	20.4	25.8	86	2	Aax54100 RANTES re
4	20.4	25.8	86	3	Aaa33544 Low adeno
5	20.4	25.8	86	3	Aaf19666 Human MIP
6	20.4	25.8	86	10	Abz5360 Human mac
7	19.8	25.1	90	2	Aat69848 Open circ
8	19.8	25.1	93	6	Abq90817 M. capsul
9	19.6	24.8	86	11	Abd19391 Human RAN
10	19.4	24.6	97	9	Ada22018 HGF aptam
11	19.2	24.3	51	3	Aac10528 Human sec
12	19.2	24.3	80	12	Adm79864 DNA ligan
13	19.2	24.3	87	8	Abx51458 Bovine ES
14	19	24.1	65	4	Aah68997 Human cer
15	19	24.1	97	14	Adx69632 Human Gnt
16	19	24.1	97	14	Adz59082 Human Gnt
17	18.8	23.8	39	2	Aav56769 Human Fac
18	18.8	23.8	72	6	Aad30987 Schizosac

C	19	18.8	23.8	72	6	AAD31044	Aad31044 Oligonucl
	20	18.8	23.8	79	4	AAF70953	Aaf70953 BFGF DNA
	21	18.8	23.8	80	2	AAT00367	Aat00367 Family 4
C	22	18.6	23.5	55	3	AAA09070	Aaa09070 Sense pri
C	23	18.6	23.5	65	6	ABN31245	Abn31245 Rat splic
C	24	18.6	23.5	80	12	ADM95117	Adm95117 Rat antis
C	25	18.6	23.5	94	4	AAI26680	Aai26680 Probe #16
C	26	18.6	23.5	94	4	ABA74927	Aba74927 Human foe
C	27	18.6	23.5	94	4	AAI55452	Aai55452 Probe #24
C	28	18.6	23.5	94	4	ABA39617	Aba39617 Probe #18
C	29	18.6	23.5	94	4	AAK49572	Aak49572 Human bon
C	30	18.6	23.5	94	4	AAK23422	Aak23422 Human bra
C	31	18.6	23.5	94	4	ABS49195	Ab49195 Human liv
C	32	18.6	23.5	94	6	ABS23058	Ab23058 Human gen
C	33	18.6	23.5	98	12	ADG99544	Adg99544 Kidney di
C	34	18.6	23.5	100	8	ACD73164	Act73164 E. coli K
C	35	18.4	23.3	62	2	AAX59388	Aax59388 Saccharom
C	36	18.4	23.3	65	3	AAC11731	Aac11731 Human sec
C	37	18.4	23.3	80	12	ADP49484	Adp49484 Oligonucl
C	38	18.4	23.3	81	4	AAL24704	Aal24704 Human bre
C	39	18.4	23.3	82	4	AAL24473	Aal24473 Human bre
C	40	18.4	23.3	90	6	ABK36475	Abk36475 HCV DNA e
C	41	18.4	23.3	93	4	AAH71852	Aah71852 Human cer
C	42	18.4	23.3	93	4	AAH68985	Aah68985 Human cer
C	43	18.4	23.3	94	4	AAH72271	Aah72271 Human cer
C	44	18.2	23.0	50	13	ADU25177	Adu25177 Retroelem
C	45	18.2	23.0	50	13	ADU22644	Adu22644 Human tra

ALIGNMENTS

RESULT 1
AAH68919
ID AAH68919 standard; cDNA; 97 BP.

AC AAH68919;

DT 19-SEP-2001 (first entry)

DE Human cervical cancer marker nucleic acid 193.

XX Cervical cancer; cytostatic; pre-malignant condition; gene therapy; ss.

OS Homo sapiens.

PN WO200142467-A2.

PD 14-JUN-2001.

PF 08-DEC-2000; 2000WO-US033312.

PR 08-DEC-1999; 99US-0169681P.
PR 21-DEC-1999; 99US-0171350P.
PR 12-MAR-2000; 2000US-018931SP.
PR 14-MAY-2000; 2000US-0203791P.
PR 09-JUN-2000; 2000US-0210600P.
PR 21-JUL-2000; 2000US-0220114P.
(MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.

PI Schlegel R, Deeds J, Berger A, Zhao X;

DR WPI; 2001-375006/39.

XX New isolated nucleic acid for diagnosing and treating cervical cancer and
PT for assessing and detecting compounds for treating the cancer.

PS Claim 1; Page 137; 1051pp; English.

CC The invention relates to novel genes (AAH68727-AAH73383) associated with
CC cervical cancer with cytostatic activity. The nucleic acids and encoded
CC polypeptides are useful: to assess if a patient is afflicted with

XX Nyce JW;
XX WPI; 2000-679539/66.
XX
XX Low adenosine (A) content antisense oligonucleotides which do not trigger
XX adenosine receptors during metabolism, useful e.g. for treating cancers
XX and respiratory obstructions.
XX
XX Claim 14; Page 219; 1592pp; English.
XX
XX The present invention describes low adenosine (A) content antisense
XX oligonucleotides and compositions (I) comprising them. In the antisense
XX oligonucleotides the A is replaced by a 'Universal' or alternative base.
XX (I) can have respiratory, bronchodilator, antiinflammatory, analgesic,
XX immunosuppressive, antiasthmatic, hypotensive and cytostatic activities.
XX The antisense oligonucleotides and (I) can be used to down-regulate the
XX expression and or activity of target polypeptides associated with
XX lung/respiratory disorders and malignancies, such as stimulating and
XX activating peptide factors and transmitters, transcription factors,
XX immunoglobulins and antibodies, antibody receptors, cytokines and
XX chemokines, endogenously produced specific and non-specific enzymes,
XX binding proteins, adhesion molecules and their receptors, cytokine and
XX chemokine receptors, adenosine receptors, bradykinin receptors, central
XX nervous system (CNS) and peripheral nervous and non-nervous system
XX receptors, CNS and peripheral nervous and non-nervous system peptide
XX transmitters, defensins, growth factors, vasoactive peptides and
XX receptors, binding proteins and malignancy associated proteins. The
XX antisense oligonucleotides may be used in this way to treat disorders
XX including respiratory obstruction (especially pulmonary obstruction
XX and/or bronchoconstriction) and/or lung inflammation, allergy(ies) and/or
XX surfactant hypo-production which are associated with a disease or
XX condition selected from pulmonary vasoconstriction, inflammation,
XX allergies, asthma, impeded respiration, respiratory distress syndrome
XX (RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary
XX hypertension, emphysema, chronic obstructive pulmonary disease (COPD),
XX pulmonary transplantation rejection, pulmonary infections, bronchitis,
XX and/or cancer. AAF18434 to AAF21543 represent human polynucleotide
XX fragments and antisense oligonucleotides used in the exemplification of
XX the present invention
XX
XX Sequence 86 BP; 0 A; 26 C; 26 G; 19 T; 0 U; 15 Other;
XX
XX Query Match 25.8%; Score 20.4; DB 3; Length 86;
XX Best Local Similarity 38.6%; Pred. No. 2.9e+03;
XX Matches 27; Conservative 17; Mismatches 26; Indels 0; Gaps 0;
QY 4 GGGCGGGGAGACGAGCGGCGUCUGGCCCCUUAUUGUACUUCGGGCGCUUAUUGUCUC 63
DB 1 GBGGGGGCGCBGTTGGGCCCCBBBGGCCCTCTCGTTCCCTTCGTTCBCTTCGTCGCGGTGCBT 60
QY 64 UCCUUUCGCC 73
DB 61 CCCCBTBTGC 70
RESULT 6
ID ABZ95360
XX ABZ95360 standard; DNA; 86 BP.
XX
XX ABZ95360;
XX
XX 17-OCT-2003 (first entry)
XX
XX Human macrophage inflammatory protein-1-alpha fragment no.1224.
XX
XX Human; antisense; lung dysfunction; nasal airway dysfunction;
XX antiinflammatory steroid; ubiquinone; antiinflammatory; antiasthmatic;
XX antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
XX antisense gene therapy; respiratory; lung; adenosine sensitivity;
XX adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
XX lung inflammation; respiratory disease; ds.
XX

OS Homo sapiens.
XX
XX WO200285308-A2.
XX
XX 31-OCT-2002.
XX
XX 23-APR-2002; 2002WO-US013135.
XX
XX 24-APR-2001; 2001US-0286137P.
XX
XX (EPIG-) EPIGENESIS PHARM INC.
XX
XX Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
XX Miller S, Tang L, Shahabuddin S;
XX WPI; 2003-229219/22.
XX
XX Pharmaceutical composition for treating ailments associated with impaired
XX respiration, has oligo(s) antisense to specific gene(s) or its
XX corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
XX ubiquinone.
XX
XX Disclosure; SEQ ID NO 10602; 872pp; English.
XX
XX The invention relates to a novel pharmaceutical composition, which has a
XX first active agent comprising an oligonucleotide antisense to the
XX initiation codon, coding region, 5' or 3' end genomic flanking regions,
XX 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
XX junctions of genes encoding a polypeptide associated with lung and/or
XX nasal airway dysfunction and a second active agent comprising an
XX antiinflammatory steroid and ubiquinone. A composition of the invention
XX has antiinflammatory, antiasthmatic, antiasthmatic, hypotensive,
XX immunosuppressive, and cytostatic activity. The composition may have a
XX use in antisense gene therapy. The composition is useful for treating or
XX preventing a respiratory, lung or malignant disease or condition, also
XX for enhancing the prophylactic or therapeutic respiratory effect of an
XX antiinflammatory steroid in a subject, for reducing or depleting levels
XX of, or reducing sensitivity to adenosine, reducing levels of adenosine
XX receptor, producing bronchodilation, increasing levels of ubiquinone or
XX lung surfactant in a subject's tissue, or treating bronchoconstriction,
XX lung inflammation, lung allergies, or a respiratory disease or condition.
XX Note: The sequence data for this patent is not represented in the printed
XX specification, but was obtained in electronic format directly from WIPO
XX at ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 86 BP; 0 A; 26 C; 26 G; 19 T; 0 U; 15 Other;
XX
XX Query Match 25.8%; Score 20.4; DB 10; Length 86;
XX Best Local Similarity 38.6%; Pred. No. 2.9e+03;
XX Matches 27; Conservative 17; Mismatches 26; Indels 0; Gaps 0;
QY 4 GGGCGGGGAGACGAGCGGCGUCUGGCCCCUUAUUGUACUUCGGGCGCUUAUUGUCUC 63
DB 1 GBGGGGGCGCBGTTGGGCCCCBBBGGCCCTCTCGTTCCCTTCGTTCBCTTCGTCGCGGTGCBT 60
QY 64 UCCUUUCGCC 73
DB 61 CCCCBTBTGC 70
RESULT 7
ID AAT69848
XX AAT69848 standard; DNA; 90 BP.
XX
XX AAT69848;
XX
XX 05-MAR-1998 (first entry)
XX
XX Open circle probe for cystic fibrosis gene.
XX
XX Open circle probe; rolling circle replication primer; mutation detection;
XX amplification target circle; unimolecular segment amplification; ss.
XX
XX multiple target detection; circular DNA; human; cystic fibrosis; ss.

RESULT 11
AAC10528/c
ID AAC10528 standard; cDNA; 51 BP.
XX AAC10528;
AC
XX
XX
DT 06-OCT-2000 (first entry)
XX
DE Human secreted protein 5' EST, SEQ ID NO: 14603.
XX
XX
KW Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;
KW gene therapy; chromosome mapping; ss.
XX
XX Homo sapiens.
XX
XX EP1033401-A2.
XX
XX 06-SEP-2000.
PD
XX
XX 21-FEB-2000; 2000EP-00200610.
PF
XX
XX 26-FEB-1999; 99US-0122487P.
PR
XX
XX (GEST) GENSET.
PA
XX
XX Dumas Milne Edwards J, Duclert A, Giordano J;
PI WPI; 2000-500381/45.
XX
XX New nucleic acid that is a 5' expressed sequence tag (5' EST) for
PT obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for
PT diagnostic, forensic, gene therapy and chromosome mapping procedures.
PT
PS Claim 1; SEQ ID NO 14603; 71pp + Sequence Listing; English.
XX
XX The present sequence is one of a large number of 5' ESTs derived from
CC mRNAs encoding secreted proteins. No ORF has yet been conclusively
CC identified within the present sequence. The 5' ESTs were prepared from
CC total human RNAs or polyA+ RNAs derived from 30 different tissues. EST
CC sequences usually correspond mainly to the 3' untranslated region (UTR)
CC of the mRNA because they are often obtained from oligo-dT primed cDNA
CC libraries. Such ESTs are not well suited for isolating cDNA sequences
CC derived from the 5' ends of mRNAs and even in those cases where longer
CC cDNA sequences have been obtained, the full 5' UTR is rarely included. 5'
CC ESTs are derived from mRNAs with intact 5' ends and can therefore be used
CC to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used in
CC diagnostic, forensic, gene therapy and chromosome mapping procedures.
CC They are used to obtain upstream regulatory sequences and to design
CC expression and secretion vectors
XX
XX Sequence 51 BP; 5 A; 23 C; 19 G; 4 T; 0 U; 0 Other;
SQ
Query Match 24.3%; Score 19.2; DB 3; Length 51;
Best Local Similarity 60.0%; Pred. No. 6.9e+03;
Matches 24; Conservative 3; Mismatches 13; Indels 0; Gaps 0;
QY 1 GGAGGCGGGGAGACGACGAGCGGCGUCUGGCCCCCUAAUU 40
DB 47 GGCGGCGGGCGGCGGCGGACGAGCGGCTCAGGCCCTGCAGT 8

RESULT 12
ADM79864
ID ADM79864 standard; DNA; 80 BP.
XX
XX
AC ADM79864;
XX
XX 03-JUN-2004 (first entry)
DT
XX
XX DNA ligand identification-related aptamer DNA sequence SeqID6.
XX

KW CE-SELEX; capillary electrophoresis; ligand-enriched mixture;
KW antiasthmatic; cerebroprotective; anti-HIV; virucide;
KW analytical chemistry; in vivo imaging; biosensor; complex matrix;
KW affinity probe capillary electrophoresis; APCE; ELISA;
KW fibre-optic microarray biosensor; histological marker;
KW tumour microvessel; anthrax spore; cocaine; ds.
XX
OS Unidentified.
OS Synthetic.
XX
XX WO2003102212-A2.
XX
PD 11-DEC-2003.
XX
XX 29-MAY-2003; 2003WO-US016796.
PF
XX
XX 31-MAY-2002; 2002US-0384709P.
PR
XX 15-MAY-2003; 2003US-0470750P.
XX
XX (MINU) UNIV MINNESOTA.
PA
XX
XX Bowser MT, Mendonsa SD;
PI WPI; 2004-043125/04.
XX
XX
XX Identifying nucleic acid ligand of target molecule from mixture
PT comprising single stranded nucleic acids having region of randomized
PT sequence by contacting mixture with target molecule, amplifying affinity
PT nucleic acids.
XX
PS Claim 27; SEQ ID NO 6; 90pp; English.
XX
XX This invention relates to a novel method (CE-SELEX, Capillary
CC Electrophoresis-Systematic Evolution of Ligands by Exponential
CC enrichment) of identifying nucleic acid ligands of a target molecule from
CC a candidate mixture comprised of single stranded nucleic acids each
CC having a region of randomized sequence by contacting the mixture with the
CC target molecule, where nucleic acids having affinity to the target
CC molecule are partitioned from the mixture by capillary electrophoresis,
CC amplifying increased affinity nucleic acids to yield a ligand-enriched
CC mixture of nucleic acids. The invention may be useful for the production
CC of compounds with an antiasthmatic, cerebroprotective, anti-HIV or
CC virucide activity. The method is useful for identifying nucleic acid
CC ligands of a target molecule from a candidate mixture comprised of single
CC stranded nucleic acids each having a region of randomized sequence.
CC Aptamers identified by the method are useful as a tool in analytical
CC chemistry, useful in wide range of diagnostic assays and as direct
CC benefits to many area of the research, including biomedical and health
CC research. Improved aptamers are useful in developing diagnostic assays,
CC for example as diagnostic markers in medical analysis, in vivo imaging
CC and biosensors. The aptamers are also useful in quantitating targets
CC present in complex matrices. The aptamers are used to develop high-
CC sensitivity affinity probe capillary electrophoresis (APCE) assays, in
CC ELISA type assays using enzyme-linked DNA aptamers. Thrombin aptamers may
CC be developed for using fibre-optic microarray biosensors. Aptamers
CC against transformed endothelial cells may be selected for use as
CC histological markers to identify tumour microvessels. Aptamers may be
CC developed for use in other aptamer-based assays, such as assays for
CC analytes ranging from anthrax spores to cocaine. Aptamers having improved
CC quality, improved binding efficiency and selectivity can be identified by
CC the method of the invention. The present sequence is that of an aptamer
CC DNA sequence which was identified using the method of the invention.
XX
SQ Sequence 80 BP; 17 A; 21 C; 21 G; 21 T; 0 U; 0 Other;

Query Match 24.3%; Score 19.2; DB 12; Length 80;
Best Local Similarity 35.9%; Pred. No. 7.5e+03;
Matches 23; Conservative 13; Mismatches 28; Indels 0; Gaps 0;
QY 6 GCGGCGGAGACGACGCGGCGUCUGGCCCCCUAAUUAGUACUUGCGGCGUCUUAUUGUCUC 65
DB 2 GCAGCACAGAGGTGCTGTTGTCACCGTTATTGCTTGCTCAGCATCCCCGCGGTAAC 61

Query Match 24.3%; Score 19.2; DB 8; Length 87;
Best Local Similarity 37.5%; Pred. No. 7.7e+03;
Matches 15; Conservative 12; Mismatches 13; Indels 0; Gaps 0;

QY 31 CCCCUAAUUGUACUCUGGCGUAGUUUGUCUCCUCCUUC 70
DB 39 CCTCTTAATTCATATCTTACTCCAATTCACTCCCTC 78

RESULT 14
AAH68997/c
ID AAH68997 standard; cDNA; 65 BP.
XX
AC AAH68997;
XX
DT 19-SEP-2001 (first entry)
XX
DE Human cervical cancer marker nucleic acid 271.
XX
KW Cervical cancer; cytostatic; pre-malignant condition; gene therapy; es.
XX
OS Homo sapiens.
XX
PN WO200142467-A2.
XX
PD 14-JUN-2001.
XX
PF 08-DEC-2000; 200WO-US033312.
XX
PR 08-DEC-1999; 99US-0169681P.
PR 21-DEC-1999; 99US-0171350P.
PR 14-MAR-2000; 2000US-0189315P.
PR 12-MAY-2000; 2000US-0203791P.
PR 09-JUN-2000; 2000US-0210600P.
PR 21-JUL-2000; 2000US-0220114P.
XX
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
XX
PI Schlegel R, Deeds J, Berger A, Zhao X;
XX WPI; 2001-375006/39.
XX
PT New isolated nucleic acid for diagnosing and treating cervical cancer and
PS for assessing and detecting compounds for treating the cancer.
XX
PS Claim 1; Page 150; 1051pp; English.

The invention relates to novel genes (AAH6897-AAH73383) associated with cervical cancer with cytosolic activity. The nucleic acids and encoded polypeptides are useful: to assess if a patient is afflicted with cervical cancer or has a pre-malignant condition; to monitor the progression of cervical cancer or a premalignant condition in a patient; and to select and/or assess the efficacy of a compound or therapy for inhibiting cervical cancer in a patient. The nucleic acids may also be useful for gene therapy

SQ Sequence 65 BP; 19 A; 17 C; 19 G; 4 T; 0 U; 6 Other;
Query Match 24.1%; Score 19; DB 4; Length 65;
Best Local Similarity 37.5%; Pred. No. 8.5e+03;
Matches 15; Conservative 10; Mismatches 15; Indels 0; Gaps 0;

QY 40 UGUACUUGGGCGUAGUUUGUCUCCUCCUCCUCCUCC 79
DB 44 TTTTCTGTGTCNTCGAANANTCTCTTCTGCTNNGGCC 5

RESULT 15
ADX69632
ID ADX69632 standard; DNA; 97 BP.
XX
AC ADX69632;

Sequence 87 BP; 28 A; 28 C; 3 G; 28 T; 0 U; 0 Other;

XX 05-MAY-2005 (first entry)
XX DE Human GntIII mutagenic forward PCR primer 1-97.
XX KW Antibody engineering; radioimmunotherapy;
KW antibody-dependent cellular toxicity;
KW n-acetyl glucosaminyl transferase III; ss; PCR; primer; Cytostatic;
KW immunotherapy; tumor; neoplasm; multiple myeloma; hematological disease;
KW immune disorder.
XX OS Homo sapiens.
OS Synthetic.
XX PN WO2005014651-A1.
XX PD 17-FEB-2005.
XX PF 11-AUG-2004; 2004WO-JP011812.
XX PR 11-AUG-2003; 2003JP-00207165.
XX PA (CHUS) CHUGAI SEIYAKU KK.
XX PI Tsuchiya M, Iijima S, Sugo I, Sugimoto M;
XX WPI; 2005-173081/18.
XX DR Anti-HM1.24 antibody useful for diagnosis of a tumor and useful as a
XX PT therapeutic agent for treating myeloma, comprises a modified sugar chain.
XX PS Example 9; SEQ ID NO 2; 58pp; Japanese.
XX CC The invention relates to an anti-HM1.24 (I) antibody which has a modified
XX CC sugar chain. Also included are an antibody composition, containing (I) in
XX CC which the sugar chain does not contain fucose and the relative ratio of
XX CC the sugar chain is 30% or more and producing the antibody. The modified
XX CC antibody is produced by culturing a host cell in which the ability of the
XX CC cell to add fucose in the sugar chain of the antibody, is deleted, and in
XX CC which the nucleic acid encoding the anti-HM1.24 antibody is introduced,
XX CC by culturing a host cell in which nucleic acid encoding N-acetyl
XX CC glucosamine transferase III (GntIII) is introduced, or by culturing a
XX CC host cell having both deleted fucose addition ability and ability to
XX CC express N-acetyl glucosamine transferase III, and extracting the antibody
XX CC from the cultured solution. The antibody does not contain alpha-1,6 core
XX CC fucose and/or has a sugar chain having a bisecting N-acetylglucosamine
XX CC (GlcNAc) structure. The modified antibody is useful for diagnosis of a
XX CC tumor and is useful as a therapeutic agent for treating myeloma such as
XX CC multiple myeloma. The antibody-dependent cellular cytotoxicity (ADCC) of
XX CC the antibody) is enhanced by the sugar chain modification. The present
XX CC sequence is a PCR primer used to produce a mutant GntIII DNA.
XX SQ Sequence 97 BP; 15 A; 34 C; 16 G; 32 T; 0 U; 0 Other;
Query Match 24.1%; Score 19; DB 14; Length 97;
Best Local Similarity 38.8%; Pred. No. 9.2e+03;
Matches 26; Conservative 11; Mismatches 30; Indels 0; Gaps 0;
QY 12 GAGAGACGACGCGCUCUGGCCCUUAUUGUACUGCGGCUUGUUCUCUCUUGCG 71
DB 3 GAGACGCTACAGCTCTTTCTCTGATGTCGTATGCGCGCGCTGCTCATCTCTCTCT 62
QY 72 CCACCUC 78
DB 63 GCACCTC 69

Search completed: October 16, 2006, 14:32:17
Job time : 305 secs

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GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioceleration Ltd.
OM nucleic - nucleic search, using sw model
Run on: October 16, 2006, 14:23:36 ; Search time 4326 Seconds
(without alignments)
1021.181 Million cell updates/sec

Title: US-10-604-726A-5135
Perfect score: 79
Sequence: 1 ggaaggcgaggagacga.....ucucuccuuccaccucc 79
Scoring table: IDENTITY_NUC
Gapop 10_0 , Gapext 1.0

Searched: 48236798 seqs, 2795665780 residues
Total number of hits satisfying chosen parameters: 853524

Minimum DB seq length: 0
Maximum DB seq length: 100

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*

1: gb_est1:*
2: gb_est3:*
3: gb_est4:*
4: gb_est5:*
5: gb_est6:*
6: gb_hic:*
7: gb_est3:*
8: gb_est7:*
9: gb_est8:*
10: gb_est9:*
11: gb_ges1:*
12: gb_ges2:*
13: gb_ges3:*
14: gb_ges4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	21.6	27.3	76	4	EX728792
2	21.2	26.8	84	1	AA414137
3	21.2	26.8	91	1	AI583881
4	20.8	26.3	91	1	AI269698
5	20.6	26.1	100	3	BQ382202
6	20.2	25.6	85	7	BF147704
7	20.2	25.6	100	1	AI616438
8	20.2	25.3	81	12	CC183143
9	20.2	25.3	88	10	H55638
10	19.8	25.1	78	14	CT351516
11	19.8	25.1	83	13	CW115558
12	19.8	25.1	83	13	CW115559
13	19.6	24.8	71	13	CW020424
14	19.6	24.8	84	10	DT921192
15	19.6	24.8	85	1	AJ649396
16	19.6	24.8	89	1	AA437593
17	19.6	24.8	100	11	AZ769498
18	19.4	24.6	58	14	CR076775
19	19.4	24.6	71	9	DN441479

20	19.4	24.6	76	11	BZ381406
21	19.4	24.6	76	13	CW236987
22	19.4	24.6	78	10	H25883
23	19.4	24.6	84	13	CW067844
24	19.4	24.6	94	7	AV957037
25	19.4	24.6	100	8	CO167293
26	19.2	24.3	46	1	AI360975
27	19.2	24.3	50	1	AU105862
28	19.2	24.3	66	13	CW022621
29	19.2	24.3	78	14	DX045680
30	19.2	24.3	79	1	AI539851
31	19.2	24.3	89	13	DU099947
32	19.2	24.3	89	13	DU108469
33	19.2	24.1	51	14	BR289701
34	19.2	24.1	78	8	CR587313
35	19.2	24.1	79	11	AZ605020
36	19.2	24.1	85	11	AZ770277
37	19.2	24.1	91	1	AA691640
38	19.2	24.1	92	2	BM157107
39	19.2	24.1	98	6	AK192966
40	18.8	23.8	46	1	AA569383
41	18.8	23.8	61	4	CB046583
42	18.8	23.8	67	10	DY248960
43	18.8	23.8	73	5	CD945332
44	18.8	23.8	78	2	BU029975
45	18.8	23.8	88	5	CF028477

ALIGNMENTS

RESULT 1
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

76 bp mRNA linear EST 18-NOV-2003
BX728792 XGC-tadpole Xenopus tropicalis cDNA clone TTPA036j08 5',
mRNA sequence.
BX728792.1 GI:38401533
EST.
Xenopus tropicalis (western clawed frog)
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;
Xenopodinae; Xenopus; Silurana.
1 (bases 1 to 76)
Croning,M.D.R., Ashurst,J.L., Taylor,R., Zorn,A.M. and Rogers,J.
Sanger Xenopus tropicalis EST project 2001 (11_2003)
Unpublished (2003)
Contact: Croning MDR
Sanger Institute
Hinxton, Cambridgeshire, CB10 1SA, UK
Email: trop@sanger.ac.uk
Sanger Xenopus tropicalis EST project 2001
TROPICALIS_SEQUENCE ID: TTPA036j08.plkSP6
Sequencing primer: SP6
This sequence is from a Xenopus Gene Collection (XGC) library
constructed by Nigel Garrett.
cDNA was oligo dt primed from 5ug of poly A+ RNA from tadpole
embryos. EcoRI-NotI cut cDNA was then ligated into pCS107 with
EcoRI at the 5' end and NotI at the 3' end.
Vector: pCS107; Site_1: EcoRI; Site_2: NotI
Host: Escherichia coli DH10B.
Location/Qualifiers
1..76
/organism="Xenopus tropicalis"
/mol_type="mRNA"
/db_xref="taxon:8364"
/clone="TTPA036j08"
/dev_stage="tadpole (stage 35-40)"
/lab_host="E. coli DH10B"
/clone_lib="XGC-tadpole"
/note="Vector: pCS107; Site_1: EcoRI; Site_2: NotI; cDNA
was oligo dt primed from 5ug of poly A+ RNA from tadpole

TITLE


```

RESULT 9
H55638/c
LOCUS
DEFINITION   CHR220577 Chromosome 22 exon Homo sapiens cDNA clone C22_783 5',
              mRNA sequence.
ACCESSION   H55638
VERSION     H55638.1  GI:1108504
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
             Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
             Homnidae; Homo.
REFERENCE   1 (bases 1 to 88)
AUTHORS    Trofatter,J.A., Long,K.R., Murrell,J.R., Stotler,C.J., Gusella,J.F.
            and Buckler,A.J.
TITLE      An expression-independent catalog of genes from human chromosome 22
JOURNAL    Genome Res. 5 (3), 214-224 (1995)
PUBMED     8593609
COMMENT    Contact: Buckler AJ
            Molecular Neurogenetics Unit
            Massachusets General Hospital
            Building 149, 13th St., Charlestown MA 02129
            Tel: 6177249616
            Fax: 6177265736
            Email: buckler@helix.mgh.harvard.edu
            Seq primer: T3.

FEATURES             Location/Qualifiers
     source           1..88
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="C22_783"
                     /lab_host="E. coli DH5a"
                     /clone_lib="Chromosome 22 exon"
                     /notes="Vector: pBluescriptKS+; Site1: Sal I; Site 2:
                     Bam HI (destroyed); Exons were isolated from human
                     chromosome 22 specific cosmids using a modification of
                     the method of exon amplification (Proc. Natl. Acad. Sci.
                     USA 88:4005-4009, 1991). Amplified exons were digested
                     with Sal I and Bgl II and subsequently cloned into
                     pBluescriptKS+ at the Sal I and Bam HI sites."

ORIGIN
Query Match      25.3%; Score 20; DB 10; Length 88;
Best Local Similarity 44.4%; Pred. No. 5.8e+04;
Matches 16; Conservative 10; Mismatches 10; Indels 0; Gaps 0;

Qy
28 UGCGCCCUAAUUGUACUUGCGGCGUAGUUGUCUC 63
      |||||:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db
70 TGTGACCCCTAATTGTTCTTCTGCTGCTCTAATAGTCTC 35

RESULT 10
CT351516/c
LOCUS
DEFINITION   Sus scrofa genomic clone CH242-438014, genomic survey sequence.
ACCESSION   CT351516
VERSION     CT351516.1  GI:79928188
KEYWORDS    GSS.
SOURCE      Sus scrofa (pig)
ORGANISM    Sus scrofa
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
             Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
             Sus.
REFERENCE   1 (bases 1 to 78)
AUTHORS    Humphray,S.J., Plumb,R.W. and Durham,J.L.
TITLE      Direct Submission
JOURNAL    Submitted (01-NOV-2005) The Sanger Institute, Wellcome Trust Genome
            Campus, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
            humquery@sanger.ac.uk Unpublished

COMMENT    This sequence was generated from the T7 end of BAC 438014. 438014
is part of the CHORI-242 BAC Library created by P. de Jong. Further
details: http://www.sanger.ac.uk/projects/S_scrofa/.

FEATURES             Location/Qualifiers
     source           1..78
                     /organism="Sus scrofa"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9823"
                     /clone="CH242-438014"
                     /tissue_type="White blood cells"
                     /note="Vector pTARBAC1.3_BamHI
                     sex female"

ORIGIN
Query Match      25.1%; Score 19.8; DB 14; Length 78;
Best Local Similarity 38.3%; Pred. No. 6.8e+04;
Matches 18; Conservative 12; Mismatches 17; Indels 0; Gaps 0;

Qy
33 CCUUAUUGUACUUGCGGCGUAGUUGUCUCUCCUCCUCCACCUCC 79
      |||||:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db
47 CATGAATGATTTAGAGCTGCTTTTGCGAGCTTCTTAGGCGCGCTCC 1

RESULT 11
CW115558/c
LOCUS
DEFINITION   104 490 11106626 116 34591.001 Sorghum methylation filtered library
              (LibID: 104) Sorghum bicolor genomic clone 11106626, genomic survey
              sequence.
ACCESSION   CW115558
VERSION     CW115558.1  GI:54808105
KEYWORDS    GSS.
SOURCE      Sorghum bicolor (sorghum)
ORGANISM    Sorghum bicolor
             Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
             Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACAD
             clade; Panicoideae; Andropogoneae; Sorghum.
REFERENCE   1 (bases 1 to 83)
AUTHORS    Bedell,J.A., Budiman,M.A., Nunberg,A., Citek,R.W., Robbins,D.,
            Jones,J., Flick,E., Rohlfing,T., Fries,J., Bradford,K.,
            McMenamy,J., Smith,M., Holeman,H., Roe,B.A., Wiley,G., Korf,I.F.,
            Rabinowicz,P.D., Lakey,N., McCombie,W.R., Jeddelloh,J.A. and
            Martienssen,R.A.
TITLE      Sorghum genome sequencing by methylation filtration
JOURNAL    PLoS Biol. 3 (1), e13 (2005)
PUBMED     15660154
COMMENT    Contact: Bedell JA
            Orion Genomics, LLC
            4041 Forest Park Ave, St. Louis, MO 63108, USA
            Tel: 314 615 6979
            Fax: 314 615 5975
            Email: jbedell@oriongenomics.com
            Plate: 490 row: o column: 02
            Seq primer: T3 Reverse
            Class: methylation filtered
            High quality sequence stop: 83.

FEATURES             Location/Qualifiers
     source           1..83
                     /organism="Sorghum bicolor"
                     /mol_type="genomic DNA"
                     /cultivar="Arix823"
                     /db_xref="taxon:4558"
                     /clone="11106626"
                     /clone_lib="Sorghum methylation filtered library (LibID:
                     104)"
                     /note="Organ: leaf; Vector: pBCSK(-); Site_1: HincII; DNA
                     prepared from purified nuclei was randomly sheared,
                     end-repaired, size fractionated to enrich for the 0.5 to 5
                     kb fraction, ligated into HincII-digested pBCSK(-) vector
                     and electroporated into E. coli cells. This is a
                     methylation filtered library."

ORIGIN

```

```

Query Match      25.1%; Score 19.8; DB 13; Length 83;
Best Local Similarity 44.4%; Pred. No. 6.8e+04;
Matches 28; Conservative 8; Mismatches 27; Indels 0; Gaps 0;

QY 2 GAGGGCGGGGAGAGACGAGCGGCGUCUGGCCCUAAUUGUACUUCGGCGGCUUAUUGUC 61
   ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 67 GAAGACGGCCCTCATCGGGCCCAACCTGGACCCCTAAATAGGAGAGCGCGCTCGTCAGGTT 8

QY 62 UCU 64
   :|:
Db 7 TCT 5

RESULT 12
CWL15559
LOCUS
DEFINITION
  104_490_11106626_148_34587_001 Sorghum methylation filtered library
  (LibID: 104) Sorghum bicolor genomic clone 11106626, genomic survey
  sequence.
ACCESSION
  CWL15559
VERSION
  GSS.
KEYWORDS
  Sorghum bicolor (sorghum)
ORGANISM
  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
  Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
  clade; Panicoideae; Andropogoneae; Sorghum.
  1 (bases 1 to 83)
Jones,J.A., Budiman,M.A., Nunberg,A., Citek,R.W., Robbins,D.,
Bedell,J.A., Flick,E., Rohlfing,T., Fries,J., Bradford,K.,
McMenamy,J., Smith,M., Holeman,H., Roe,B.A., Wiley,G., Korf,I.F.,
Rabinowicz,P.D., Lakey,N., McCombie,W.R., Jeddeloh,J.A. and
Martensen,R.A.
Sorghum genome sequencing by methylation filtration
PLOS Biol. 3 (1), e13 (2005)
15660154
Contact: Bedell JA
Orion Genomics, LLC
4041 Forest Park Ave, St. Louis, MO 63108, USA
Tel: 314 615 6979
Fax: 314 615 5975
Email: jbedell@oriongenomics.com
Plate: 490 row: 0 column: 02
Seq primer: Sfor Forward
Class: methylation filtered
High quality sequence stop: 83.
Location/Qualifiers
  1..83
  /organism="Sorghum bicolor"
  /mol_type="genomic DNA"
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  /clone="11106626"
  /clone_lib="Sorghum methylation filtered library (LibID:
  104)"
  /notes="Organ: Leaf; Vector: pBCSK(-); Site 1: HincII; DNA
  prepared from purified nuclei was randomly sheared,
  end-repaired, size fractionated to enrich for the 0.5 to 5
  kb fraction, ligated into HincII-digested pBCSK(-) vector
  and electroporated into E. coli cells. This is a
  methylation filtered library."

FEATURES
  source
  1..83
  /organism="Sorghum bicolor"
  /mol_type="genomic DNA"
  /cultivar="RTx623"
  /db_xref="taxon:4558"
  /clone="11106626"
  /clone_lib="Sorghum methylation filtered library (LibID:
  104)"
  /notes="Organ: Leaf; Vector: pBCSK(-); Site 1: HincII; DNA
  prepared from purified nuclei was randomly sheared,
  end-repaired, size fractionated to enrich for the 0.5 to 5
  kb fraction, ligated into HincII-digested pBCSK(-) vector
  and electroporated into E. coli cells. This is a
  methylation filtered library."

ORIGIN
  Query Match      25.1%; Score 19.8; DB 13; Length 83;
  Best Local Similarity 44.4%; Pred. No. 6.8e+04;
  Matches 28; Conservative 8; Mismatches 27; Indels 0; Gaps 0;

QY 2 GAGGGCGGGGAGAGACGAGCGGCGUCUGGCCCUAAUUGUACUUCGGCGGCUUAUUGUC 61
   ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 15 GAAGACGGCCCTCATCGGGCCCAACCTGGACCCCTAAATAGGAGAGCGCGCTCGTCAGGTT 74

QY 62 UCU 64
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Db 75 TCT 77

RESULT 13
CWL20424
LOCUS
DEFINITION
  71 bp mRNA linear GSS 28-SEP-2004
  GC0686 TIGEM gene trap library Mus musculus cDNA clone A011.G4,
  mRNA sequence.
ACCESSION
  CWL20424
VERSION
  CWL20424.1 GI:52789684
KEYWORDS
  GSS.
SOURCE
  Mus musculus (house mouse)
ORGANISM
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
  Sciurognathi; Muroidea; Muridae; Murinae; Mus.
  1 (bases 1 to 71)
Cobellis,G., Niclaus,G., Iovino,M., Romito,A., Marra,E.,
Barbarisi,M., Sardiello,M., Di Giorgio,F.P., Iovino,N., Zollo,M.,
Ballabio,A. and Cortese,R.
Tagging genes with cassette-exchange sites
Nucleic Acids Res. 33 (4), e44 (2005)
15741177
Contact: TIGEM
107
TIGEM
Via P. Castellino, 111, 80131 NAPOLI, ITALY
Tel: +390816132205
Fax: +390815790919
Email: cobellis@tigem.it
Sequence tag generated by 5' RACE of total RNA from gene trap ES
cell line. ES cell lines harboring insertion mutation of target
gene are available upon request from TIGEM. Annotation information
available from TIGEM
Class: Gene trap.
Location/Qualifiers
  1..71
  /organism="Mus musculus"
  /mol_type="mRNA"
  /strain="129 Ola"
  /db_xref="taxon:10090"
  /clone="A011.G4"
  /sex="male"
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  /cell_line="E14"
  /clone_lib="TIGEM gene trap library"
  /note="Vector: pFLIPl"

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  Best Local Similarity 52.0%; Pred. No. 7.8e+04;
  Matches 26; Conservative 5; Mismatches 19; Indels 0; Gaps 0;

QY 1 GGAGCGCGGGGAGAGACGAGCGGCGUCUGGCCCUAAUUGUACUUCGGG 50
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Db 1 GGGGGGGGGGAAAAACGGGGGGGGCCCCCCTTTTATACAGGGGG 50

RESULT 14
CWL21192/c
LOCUS
DEFINITION
  84 bp mRNA linear EST 19-SEP-2005
  PCS50390_2 Hematopoietic stem cells Mus musculus cDNA, mRNA
  sequence.
ACCESSION
  CWL21192
VERSION
  CWL21192.1 GI:75901673
KEYWORDS
  EST.
SOURCE
  Mus musculus (house mouse)
ORGANISM
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
  Sciurognathi; Muroidea; Muridae; Murinae; Mus.
  1 (bases 1 to 84)
Pritsker,M., Doniger,T.T., Kramer,L.C., Westcot,S.E. and

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TITLE Lemischka, I.R.
JOURNAL Diversification of Stem Cell Molecular Repertoire by Alternative
COMMENT Splicing
Proc. Natl. Acad. Sci. U.S.A. (2005) In press
Contact: Pritsker M
Lab of Thor Lemischka, Department of Molecular Biology
Princeton University
Princeton, NJ 08544, USA
Tel: 609 258 5657
Fax: 609 258 1704
Email: pritaker@molbio.princeton.edu.

FEATURES
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/tissue_type="Hematopoietic stem cells"
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/note="cDNA library was made from FACS-purified
hematopoietic stem cells"

ORIGIN

Query Match 24.8%; Score 19.6; DB 10; Length 84;
Best Local Similarity 36.2%; Pred. No. 8e+04;
Matches 21; Conservative 13; Mismatches 24; Indels 0; Gaps 0;
QY 21 GCGGCGUCUGCCCUAAUUGUACUUGCGGCGUUAUUGUCUCUUCUGCCACCC 78
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RESULT 15
AJ649396
LOCUS AJ649396 CSEQRAN19 Sus scrofa cDNA clone C0003272_F23, mRNA
DEFINITION sequence.
ACCESSION AJ649396
VERSION AJ649396.1 GI:49326241
KEYWORDS EST.
SOURCE Sus scrofa (pig)
ORGANISM Sus scrofa

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
Sus.
1 (bases 1 to 85)
Anderson, S.I., Finlayson, H.A. and Archibald, A.L.
Development of cDNA and EST resources for studying reproduction and
embryo development in pigs and cattle
Unpublished (2004)
Contact: Anderson SI

Genomics and Bioinformatics
Roslin Institute
Roslin, Midlothian, EH25 9PS, UNITED KINGDOM
Single pass sequencing. Bases called and trimmed with phred
v0.020425.c. Vector identified by cross match with the -minscore 20
and -mismatch 12 options. Vector: pBlueScriptII (KS) R. Site1: EcoRI
R. Site2: NotI 5' Seg Primer M13F Normalised library constructed
from pooled ovaries. Clones available from UK Centre for Functional
Genomics in Farm Animals, Roslin Institute, Roslin, Midlothian, UK,
EH25 9PS, www.ark-genomics.Org.

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constructed from pooled ovaries"

ORIGIN

Query Match 24.8%; Score 19.6; DB 1; Length 85;
Best Local Similarity 42.0%; Pred. No. 8e+04;
Matches 21; Conservative 10; Mismatches 19; Indels 0; Gaps 0;
QY 16 GAGGAGCGGCGUCUGCCCGCCCUAAUUGUACUUCGGGCGUUAUUGUCUCUC 65
Db 8 GTGCGGAGCGGCTGGCGCTTCCTCGTCCCGAGTGAATGGTCTCTC 57

Search completed: October 16, 2006, 16:16:48
Job time : 4331 secs

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GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 16, 2006, 14:28:14 ; Search time 110 Seconds
(without alignments)
1343.796 Million cell updates/sec

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Perfect score: 79
Sequence: 1 ggaaggcggggagagacga.....ucucuccuuagccaccucc 79

Scoring table: IDENTITY NUC
Gapop 10_0 , Gapext 1.0

Searched: 1403666 seqs, 93554401 residues

Total number of hits satisfying chosen parameters: 1560966

Minimum DB seq length: 0
Maximum DB seq length: 100

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents NA: *
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2: /EMC_Celerra_SIDS3/ptodata/2/ina/5 COMB.seq: *
3: /EMC_Celerra_SIDS3/ptodata/2/ina/6A COMB.seq: *
4: /EMC_Celerra_SIDS3/ptodata/2/ina/6B COMB.seq: *
5: /EMC_Celerra_SIDS3/ptodata/2/ina/7 COMB.seq: *
6: /EMC_Celerra_SIDS3/ptodata/2/ina/H COMB.seq: *
7: /EMC_Celerra_SIDS3/ptodata/2/ina/PP COMB.seq: *
8: /EMC_Celerra_SIDS3/ptodata/2/ina/PP COMB.seq: *
9: /EMC_Celerra_SIDS3/ptodata/2/ina/RE COMB.seq: *
10: /EMC_Celerra_SIDS3/ptodata/2/ina/backfiles1.seq: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	20	25.3	93	3	US-09-621-976-18431
3	19.8	25.1	63	2	US-08-014-723-12
4	19.8	25.1	63	2	US-08-110-011A-12
5	19.4	24.6	97	3	US-08-952-793-288
6	19.4	24.6	97	3	US-09-849-928-288
7	19.4	24.6	97	7	PCT-US96-09455A-288
8	19.2	24.3	51	3	US-09-513-999C-14603
9	19	24.1	65	2	US-08-014-723-11
10	19	24.1	65	2	US-08-110-011A-11
11	18.8	23.8	39	3	US-09-367-791A-19
12	18.8	23.8	54	3	US-08-444-818-753
13	18.8	23.8	79	3	US-08-687-421-415
14	18.4	23.3	62	3	US-08-965-762-27
15	18.4	23.3	62	3	US-09-911-927-27
16	18.4	23.3	62	3	US-09-911-882-27
17	18.4	23.3	62	3	US-09-911-888-27
18	18.4	23.3	65	3	US-09-513-999C-15806
19	18.2	23.0	65	2	US-08-086-410-28
20	18	22.8	42	3	US-09-475-947A-86
21	18	22.8	78	2	US-08-090-193-16
22	18	22.8	78	2	US-08-488-031-16
23	18	22.8	78	2	US-08-486-569-16

C 24	18	22.8	78	2	US-08-488-027-16	Sequence 16, Appl
C 25	18	22.8	78	2	US-08-090-192-16	Sequence 16, Appl
C 26	18	22.8	78	2	US-08-482-663-16	Sequence 16, Appl
C 27	18	22.8	78	3	US-08-482-658-16	Sequence 16, Appl
C 28	18	22.8	78	3	US-08-470-349-16	Sequence 16, Appl
C 29	18	22.8	78	3	US-08-475-610-16	Sequence 16, Appl
C 30	18	22.8	78	7	PCT-US92-00277-16	Sequence 16, Appl
C 31	18	22.8	78	7	PCT-US92-00278-16	Sequence 16, Appl
C 32	17.8	22.5	77	5	US-09-844-508-25	Sequence 25, Appl
C 33	17.8	22.5	87	3	US-09-873-075A-5	Sequence 5, Appl
C 34	17.6	22.3	87	4	US-09-393-803-68	Sequence 68, Appl
C 35	17.6	22.3	50	3	US-10-131-827-847	Sequence 847, Appl
C 36	17.6	22.3	50	5	US-10-131-831-847	Sequence 847, Appl
C 37	17.6	22.3	59	2	US-08-790-963-53	Sequence 53, Appl
C 38	17.6	22.3	59	3	US-09-371-774-53	Sequence 53, Appl
C 39	17.6	22.3	59	3	US-09-875-082-53	Sequence 13, Appl
C 40	17.4	22.0	72	2	US-08-433-126A-13	Sequence 13, Appl
C 41	17.4	22.0	72	2	US-08-433-124A-13	Sequence 13, Appl
C 42	17.4	22.0	72	3	US-08-976-413A-13	Sequence 13, Appl
C 43	17.4	22.0	72	7	PCT-US96-06059-13	Sequence 13, Appl
C 44	17.4	22.0	91	3	US-09-513-999C-15862	Sequence 15862, A
C 45	17.2	21.8	54	3	US-09-621-976-13448	Sequence 13448, A

ALIGNMENTS

RESULT 1
US-09-543-679A-1233
; Sequence 1233, Application US/09543679A
; Patent No. 7034007
; GENERAL INFORMATION:
; APPLICANT: NYCE, Jonathan W.
; TITLE OF INVENTION: LOW ADENOSINE ANTI-SENSE OLIGONUCLEOTIDE,
; COMPOSITIONS, KIT & METHOD FOR TREATMENT
; OF AIRWAY DISORDERS ASSOCIATED WITH
; BRONCHOCOINCTION, LUNG INFLAMMATION,
; NUMBER OF SEQUENCES: 3111
; CORRESPONDENCE ADDRESS:
; ADDRESS: EPIGENESIS PHARMACEUTICALS, INC.
; STREET: 7 Clarke Drive
; CITY: Cranbury
; STATE: NJ
; COUNTRY: USA
; ZIP: 08512
; COMPUTER READABLE FORM:
; MEDIUM TYPE: CD-R
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: N/A
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/543,679A
; FILING DATE: 13-Apr-2000
; CLASSIFICATION: UNKNOWN
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/127,958
; FILING DATE: 1998-08-03
; ATTORNEY/AGENT INFORMATION:
; NAME: Amzel, Viviana
; REGISTRATION NUMBER: 30,930
; REFERENCE/DOCKET NUMBER: EPI-0067191b
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 609-409-3035
; TELEFAX: 413-254-9245
; TELEX: <unknown>
; INFORMATION FOR SEQ ID NO: 1233:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 86 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Genomic DNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 1233:

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US-09-543-679A-1233
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Best Local Similarity 38.6%; Pred. No. 3.6e+02;
Matches 27; Conservative 17; Mismatches 26; Indels 0; Gaps 0;

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Db 1 GBGGGGGCBGCBGTTGGGCCCCBBBGGCCCTCTCGTTCBCCCTTCTGCBGGBGTTGCBT 60

Qy 64 UCCUUGGCC 73
Db 61 CCCBtBtGC 70

RESULT 2
US-09-621-976-18431/c
; Sequence 18431, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET 054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 18431
; LENGTH: 93
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 63..64,83
; OTHER INFORMATION: n=a, g, c or t
US-09-621-976-18431

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Best Local Similarity 63.9%; Pred. No. 5.2e+02;
Matches 23; Conservative 3; Mismatches 10; Indels 0; Gaps 0;

Qy 5 GCGGGGAGACGAGCGGCGUCUGGCCCUAAU 40
Db 58 GCGGGGCGGCGACGAGCGGCTCAGGCCCTCGAGT 23

RESULT 3
US-08-014-723-12/c
; Sequence 12, Application US/08014723
; Patent No. 5273962
; GENERAL INFORMATION:
; APPLICANT: Doi, Takeshi
; APPLICANT: Iwasaki, Akio
; APPLICANT: Saino, Yushi
; APPLICANT: Kimura, Shigeru
; APPLICANT: Ohkuchi, Masao
; TITLE OF INVENTION: Thrombin-Binding Substance and Process
; TITLE OF INVENTION: For Preparing the Same
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: P.C.
; ADDRESSEE: 1755 Jefferson Davis Highway, Fourth Floor
; CITY: Arlington
; STATE: Virginia
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/110,011A
; FILING DATE: 23-AUG-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Oblon, No. 5354664man F.
; REGISTRATION/DOCKET NUMBER: 24,618
; REFERENCE/DOCKET NUMBER: 80-073-0 DIV
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703)413-3000
; TELEFAX: (703)413-2220
; TELEX: 248855 OPAT UR
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 63 bases
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear

US-08-014-723-12
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Best Local Similarity 59.0%; Pred. No. 5.6e+02;
Matches 23; Conservative 4; Mismatches 12; Indels 0; Gaps 0;

Qy 3 AGGGCGGGGAGACGAGCGGCGUCUGGCCCUAAUUG 41
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RESULT 4
US-08-110-011A-12/c
; Sequence 12, Application US/08110011A
; Patent No. 5354664
; GENERAL INFORMATION:
; APPLICANT: Doi, Takeshi
; APPLICANT: Iwasaki, Akio
; APPLICANT: Saino, Yushi
; APPLICANT: Kimura, Shigeru
; APPLICANT: Ohkuchi, Masao
; TITLE OF INVENTION: Thrombin-Binding Substance and Process
; TITLE OF INVENTION: For Preparing the Same
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: P.C.
; ADDRESSEE: 1755 Jefferson Davis Highway, Fourth Floor
; CITY: Arlington
; STATE: Virginia
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/110,011A
; FILING DATE: 23-AUG-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Oblon, No. 5354664man F.
; REGISTRATION/DOCKET NUMBER: 24,618
; REFERENCE/DOCKET NUMBER: 80-073-0 DIV
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703)413-3000
; TELEFAX: (703)413-2220
; TELEX: 248855 OPAT UR
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 63 bases
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
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QY 19 GAGCGCUCUGGCCCCUUAUUGUACUCGGGCGUCGUAUUGUCUCUCCUUGCCACCCUC 78
Db 90 GTGAGCCTCTGTGCGAATCTTACTACTTCTGCTTTGTGTTTGTTCCTTGCGTGCCCTT 31

QY 79 C 79
Db 30 C 30

RESULT 7

PCT-US96-09455A-288/c
; Sequence 288, Application PC/TUS9609455A
; GENERAL INFORMATION:
; APPLICANT: PARMA, et al.
; TITLE OF INVENTION: HIGH AFFINITY NUCLEIC ACID
; TITLE OF INVENTION: LIGANDS TO LECTINS
; NUMBER OF SEQUENCES: 390
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Swanson & Bratschun, L.L.C.
; STREET: 8400 E. Prentice Avenue, Suite 200
; CITY: Englewood
; STATE: Colorado
; COUNTRY: USA
; ZIP: 80111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3 1/2 diskette, 1.44 MB
; COMPUTER: IBM pc compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WordPerfect 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/09455A
; FILING DATE: 05 JUNE 1996
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/479,724
; FILING DATE: 07-JUNE-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/472,256
; FILING DATE: 07-JUNE-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/472,255
; FILING DATE: 07-JUNE-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/477,829
; FILING DATE: 07-JUNE-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Barry J. Swanson
; REGISTRATION NUMBER: 33,215
; REFERENCE/DOCKET NUMBER: NEX40C/PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (303) 793-3333
; TELEFAX: (303) 793-3433
; INFORMATION FOR SEQ ID NO: 288:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 97 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: RNA
; FEATURE:
; OTHER INFORMATION: All C's are 2'-NH2 cytosine
; FEATURE:
; OTHER INFORMATION: All U's are 2'-NH2 uracil
PCT-US96-09455A-288

Query Match 24.6%; Score 19.4; DB 7; Length 97;
Best Local Similarity 31.1%; Pred. No. 8.9e+02;
Matches 19; Conservative 16; Mismatches 26; Indels 0; Gaps 0;
QY 19 GAGCGCUCUGGCCCCUUAUUGUACUCGGGCGUCGUAUUGUCUCUCCUUGCCACCCUC 78
Db 90 GTGAGCCTCTGTGCGAATCTTACTACTTCTGCTTTGTGTTTGTTCCTTGCGTGCCCTT 31

QY 79 C 79
Db 30 C 30

RESULT 8

US-09-513-999C-14603/c
; Sequence 14603, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; Patent No. 6783961
; FILE REFERENCE: 59.US2.REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 14603
; LENGTH: 51
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-513-999C-14603

Query Match 24.3%; Score 19.2; DB 3; Length 51;
Best Local Similarity 60.0%; Pred. No. 8.9e+02;
Matches 24; Conservative 3; Mismatches 13; Indels 0; Gaps 0;

QY 1 GGAGGGCGGGGAGAGACGAGCGGCGUCUGGCCCCUUAUU 40
Db 47 GGGCGGCGGGCGGCGAGCAGCGGCTCAGGCCCTGCAGT 8

RESULT 9

US-08-014-723-11
; Sequence 11, Application US/08014723
; Patent No. 5273962
; GENERAL INFORMATION:
; APPLICANT: Doi, Takeshi
; APPLICANT: Iwasaki, Akio
; APPLICANT: Saino, Yushi
; APPLICANT: Kimura, Shigeru
; APPLICANT: Ohkuchi, Masao
; TITLE OF INVENTION: Thrombin-Binding Substance and Process
; TITLE OF INVENTION: For Preparing the Same
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: P.C.
; STREET: 1755 Jefferson Davis Highway, Fourth Floor
; CITY: Arlington
; STATE: Virginia
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/014,723
; FILING DATE: 19930208
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Oblon, No. 5273962man F.
; REGISTRATION NUMBER: 24,618
; REFERENCE/DOCKET NUMBER: 80-071-0 CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703)413-3000

DB 30 AGGTGACGACGAGCGCCAGCGCTCTGGCGACTGA 64

RESULT 11
US-09-367-791A-19
; Sequence 19, Application US/09367791A
; Patent No. 6573071
; GENERAL INFORMATION:
; APPLICANT: Himmelsbach, Michele
; Schlokat, Uwe
; Dörner, Friedrich
; Fisch, Andreas
; Eibl, Johann
TITLE OF INVENTION: Factor X Analogues With
; a Modified Protease Cleavage Site
NUMBER OF SEQUENCES: 122
CORRESPONDENCE ADDRESS:
ADDRESSES: Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: CA
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/367,791A
FILING DATE: 12-NO. 6573071-1999
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: AT A 335/97
FILING DATE: 27-FEB-1997
APPLICATION NUMBER: WO PCT/AT98/00045
FILING DATE: 27-FEB-1998
ATTORNEY/AGENT INFORMATION:
NAME: Ausenhus, Scott L.
REGISTRATION NUMBER: 42,471
REFERENCE/DOCKET NUMBER: 20695D-000700U5
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
TEXT: <Unknown>
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 39 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
SEQUENCE DESCRIPTION: SEQ ID NO: 19:

US-09-367-791A-19

Query Match 23.8%; Score 18.8; DB 3; Length 33
Best Local Similarity 44.7%; Pred. No. 1.2e+03;
Matches 17; Conservative 9; Mismatches 12; Indels

QY 33 CCUAUAUGUACUUCGGGCUCGUUAUGUCUCCUUUC 70
|| ||| :|||:|||::|||::|||:

DB 2 CCAAGATCATTTCTCGTGCTCGTGTTCGCCCTCTC 39

RESULT 12
US-08-444-818-753/c
; Sequence 753, Application US/08444818
; Patent No. 6150087
; GENERAL INFORMATION:
; APPLICANT: Chien, David Y.
; APPLICANT: Rutter, William J.
TITLE OF INVENTION: NANB Diagnostics and Vaccines
NUMBER OF SEQUENCES: 777

```
/
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Chiron Corporation
/ STREET: 4560 Horton Street
/ CITY: Emeryville
/ STATE: CA
/ COUNTRY: USA
/ ZIP: 94608-2916
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/444,818
/ FILING DATE:
/ CLASSIFICATION: 424
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US/08/403,590
/ FILING DATE: 14-MAR-1995
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Harbin, Alisa A.
/ REGISTRATION NUMBER: 33,895
/ REFERENCE/DOCKET NUMBER: 0110.002
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (508)359-3876
/ TELEFAX: (508)359-3885
/ INFORMATION FOR SEQ ID NO: 753:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 54 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: other nucleic acid
/ DESCRIPTION: /desc = "primer JHC 13"
/ US-08-444-818-753

Query Match 23.8%; Score 18.8; DB 3; Length 54;
Best Local Similarity 48.1%; Pred. No. 1.3e+03;
Matches 26; Conservative 6; Mismatches 22; Indels 0; Gaps 0;

QY 5 GCGGGGGGAGAGCGAGCGCGCUCUGGCCCCUUAUUGUACUUCGGCGCUGUUAU 58
Db 54 GCGGGGGGGGGGGGGTCTATAGTGTACCTAAATCGTATGGCGCGCGGAATT 1

RESULT 13
US-08-687-421-415
/ Sequence 415, Application US/08687421
/ Patent No. 6177557
/ GENERAL INFORMATION:
/ APPLICANT: Gold, Larry
/ APPLICANT: Janjic, Nebojsa
/ APPLICANT: Tasset, Diane
/ TITLE OF INVENTION: HIGH-AFFINITY LIGANDS OF BASIC
/ TITLE OF INVENTION: FIBROBLAST GROWTH FACTOR AND
/ TITLE OF INVENTION: THROMBIN
/ NUMBER OF SEQUENCES: 445
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Swanson & Brateschun, L.L.C.
/ STREET: 8400 E. Prentice Avenue, Suite 200
/ CITY: Englewood
/ STATE: Colorado
/ COUNTRY: USA
/ ZIP: 80111
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Diskette, 3.5 inch, 1.44 MB storage
/ COMPUTER: IBM compatible
/ OPERATING SYSTEM: MS-DOS
/ SOFTWARE: Wordperfect 6.0
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/687,421
/ FILING DATE: 08-MAY-1996
/ CLASSIFICATION: 435

/
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Chiron Corporation
/ STREET: 4560 Horton Street
/ CITY: Emeryville
/ STATE: CA
/ COUNTRY: USA
/ ZIP: 94608-2916
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/444,818
/ FILING DATE:
/ CLASSIFICATION: 424
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US/08/403,590
/ FILING DATE: 14-MAR-1995
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Harbin, Alisa A.
/ REGISTRATION NUMBER: 33,895
/ REFERENCE/DOCKET NUMBER: 0110.002
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (508)359-3876
/ TELEFAX: (508)359-3885
/ INFORMATION FOR SEQ ID NO: 753:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 54 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: other nucleic acid
/ DESCRIPTION: /desc = "primer JHC 13"
/ US-08-444-818-753

Query Match 23.8%; Score 18.8; DB 3; Length 79;
Best Local Similarity 38.7%; Pred. No. 1.4e+03;
Matches 24; Conservative 11; Mismatches 27; Indels 0; Gaps 0;

QY 17 ACGAGCGGCGUCUGGCCCCUUAUUGUACUUCGGCGCUGUUAUUGCACC 76
Db 7 ACGATCTGACTAGCACCTGCATAGGAGTACCGACTCCGATTGTATGTACCTAGCTTAC 66

QY 77 UC 78
Db 67 TC 68

RESULT 14
US-08-965-762-27
/ Sequence 27, Application US/08965762
/ Patent No. 6280963
/ GENERAL INFORMATION:
/ APPLICANT: Koltin, Yigal
/ APPLICANT: Gavrias, Victoria
/ TITLE OF INVENTION: ESSENTIAL FUNGAL GENES AND THEIR USE
/ FILE REFERENCE: 07334/062001
/ CURRENT APPLICATION NUMBER: US/08/965,762
/ CURRENT FILING DATE: 1997-11-07
/ NUMBER OF SEQ ID NOS: 35
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 27
/ LENGTH: 62
/ TYPE: DNA
/ ORGANISM: Saccharomyces cerevisiae
/ US-08-965-762-27

Query Match 23.3%; Score 18.4; DB 3; Length 62;
Best Local Similarity 38.5%; Pred. No. 1.9e+03;
Matches 20; Conservative 11; Mismatches 21; Indels 0; Gaps 0;

QY 27 CUGGCCCCUUAUUGUACUUCGGCGCUGUUAUUGUACUUCUUCUUCGCCACCUC 78
Db 8 CCGCGCCCATCAAGCAAGATCTCTGATGATTTGACATTCCTCTTGGCCTCTC 59
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RESULT 15

US-09-911-927-27
; Sequence 27, Application US/09911927
; Patent No. 6461826
; GENERAL INFORMATION:
; APPLICANT: Koltin, Yigal
; APPLICANT: Gavrilas, Victoria
; TITLE OF INVENTION: ESSENTIAL FUNGAL GENES AND THEIR USE
; FILE REFERENCE: 06286-062003
; CURRENT APPLICATION NUMBER: US/09/911,927
; CURRENT FILING DATE: 2001-07-23
; PRIOR APPLICATION NUMBER: US 08/965,762
; PRIOR FILING DATE: 1997-11-07
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 27
; LENGTH: 62
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: primer for PCR
US-09-911-927-27

Query Match 23.3%; Score 18.4; DB 3; Length 62;
Best Local Similarity 38.5%; Pred. No. 1.9e+03;
Matches 20; Conservative 11; Mismatches 21; Indels 0; Gaps 0;

Qy 27 CUGGCCCUUAUUGUACUUGGGCUGGUUUGUUCUCCUUGCGCACCCUC 78
Db 8 CCGCGCCCATCATGCAAGATCCTGATGGTATTGACATTCTTTGGCCTCTC 59

Search completed: October 16, 2006, 14:34:12
Job time : 111 secs

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Copyright (c) 1993 - 2006 Bioceleration Ltd.
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Run on: October 16, 2006, 14:32:38 ; Search time 881 Seconds
(without alignments)
1101.842 Million cell updates/sec
Title: US-10-604-726A-5135
Perfect score: 79
Sequence: 1 9ga9ggcg9ggagagacga.....ucucuccuucgccaccucc 79
Scoring table: IDENTITY NUC
Gapop 10_0 , Gapext 1.0
Searched: 18932170 seqs, 6143817638 residues
Total number of hits satisfying chosen parameters: 24414840
Minimum DB seq length: 0
Maximum DB seq length: 100
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications_NA_Main:*

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2: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US08_PUBCOMB.seq.*
3: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09A_PUBCOMB.seq.*
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7: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10B_PUBCOMB.seq.*
8: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10C_PUBCOMB.seq.*
9: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10D_PUBCOMB.seq.*
10: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10E_PUBCOMB.seq.*
11: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10F_PUBCOMB.seq.*
12: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10G_PUBCOMB.seq.*
13: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10H_PUBCOMB.seq.*
14: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11A_PUBCOMB.seq.*
15: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11B_PUBCOMB.seq.*
16: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11C_PUBCOMB.seq.*
17: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11D_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	27	34.2	67	11	US-10-310-914A-16611
C 2	23	29.1	87	3	Sequence 16611, A
C 3	19.4	24.6	97	3	Sequence 4883, Ap
C 4	19.4	24.6	97	6	Sequence 288, App
C 5	19.4	24.6	97	6	Sequence 288, App
C 6	19.4	24.6	97	8	Sequence 288, App
C 7	19.2	24.3	80	8	Sequence 288, App
C 8	19.2	24.3	80	8	Sequence 6, Appli
C 9	19	24.1	86	16	Sequence 1387, Ap
C 10	19	24.1	86	16	Sequence 22, Appl
C 11	18.8	23.8	24	11	Sequence 37212, A
C 12	18.8	23.8	39	7	Sequence 19, Appl
C 13	18.8	23.8	72	3	Sequence 15, Appl
C 14	18.8	23.8	72	9	Sequence 15, Appl
C 15	18.8	23.8	72	13	Sequence 15, Appl
C 16	18.6	23.5	55	10	Sequence 3, Appli
C 17	18.6	23.5	65	3	Sequence 3993, Ap

C 18	18.6	23.5	80	8	US-10-384-245-10	Sequence 10, Appl
C 19	18.6	23.5	94	3	US-09-864-761-24937	Sequence 24937, A
C 20	18.6	23.5	99	11	US-10-932-182A-173876	Sequence 173876, A
C 21	18.4	23.3	50	16	US-11-175-859-47265	Sequence 47265, A
C 22	18.4	23.3	62	3	US-09-911-888-27	Sequence 27, Appl
C 23	18.4	23.3	62	3	US-09-911-927-27	Sequence 27, Appl
C 24	18.4	23.3	62	3	US-10-296-734-485	Sequence 485, App
C 25	18.4	23.3	94	11	US-10-310-914A-15206	Sequence 15206, A
C 26	18.2	23.0	50	16	US-11-175-859-73819	Sequence 73819, A
C 27	18.2	23.0	60	3	US-09-908-975-10452	Sequence 10452, A
C 28	18.2	23.0	63	9	US-10-819-095-9	Sequence 9, Appli
C 29	18.2	23.0	65	3	US-09-908-975-931	Sequence 931, App
C 30	18.2	23.0	90	8	US-10-296-734-314	Sequence 314, App
C 31	18	22.8	80	8	US-10-384-245-343	Sequence 343, App
C 32	18	22.8	80	8	US-10-296-734-288	Sequence 288, App
C 33	17.8	22.5	24	11	US-10-310-914A-914124	Sequence 914124, A
C 34	17.8	22.5	77	3	US-09-844-508-25	Sequence 25, Appl
C 35	17.8	22.5	77	6	US-10-084-826-25	Sequence 25, Appl
C 36	17.8	22.5	87	3	US-09-873-075A-5	Sequence 5, Appli
C 37	17.8	22.5	87	16	US-11-115-425-68	Sequence 68, Appl
C 38	17.8	22.5	100	3	US-09-728-445-363	Sequence 363, App
C 39	17.8	22.5	100	10	US-10-964-549-363	Sequence 363, App
C 40	17.6	22.3	25	13	US-11-036-317-296412	Sequence 296412, A
C 41	17.6	22.3	25	13	US-11-036-317-372387	Sequence 372387, A
C 42	17.6	22.3	25	13	US-11-036-317-976170	Sequence 976170, A
C 43	17.6	22.3	50	7	US-10-131-827-847	Sequence 847, App
C 44	17.6	22.3	50	16	US-11-175-859-8102	Sequence 8102, Ap
C 45	17.6	22.3	50	16	US-11-175-859-29840	Sequence 29840, A

ALIGNMENTS

RESULT 1
US-10-310-914A-16611/c
; Sequence 16611, Application US/10310914A
; Publication No. US2006000322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiller, Kuvzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 16611
; LENGTH: 67
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-16611

Query Match	34.2%	Score 27;	DB 11;	Length 67;
Best Local Similarity	80.0%;	Pred. No. 6.8;		
Matches	28;	Conservative	2;	Mismatches 5; Indels 0; Gaps 0;
QY	1	GGAGGGCGGGGAGAGAGCGAGCGGCGUCUGGCCCCU	35	
DB	67	GGAGGGCTGGGAGAGAGAGAGCCCTGGCCCT	33	

RESULT 2
US-09-294-093B-4883/c
; Sequence 4883, Application US/09294093B
; Patent No. US20010051335A1
; GENERAL INFORMATION:
; APPLICANT: Ialugdi, Raghunath, V.
; APPLICANT: Ito, Laura, Y.
; APPLICANT: Sherman, Bradley, K.
; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN TASSEL
; FILE REFERENCE: PL-0009 US
; CURRENT APPLICATION NUMBER: US/09/294,093B

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; CURRENT FILING DATE: 1999-04-16
; PRIOR APPLICATION NUMBER: 60/082,567
; PRIOR FILING DATE: April 21, 1998
; NUMBER OF SEQ ID NOS: 6207
; SOFTWARE: PERL Program
; SEQ ID NO 4883
; LENGTH: 87
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20010051335A1 700355274H1
; NAME/KEY: unsure
; LOCATION: 32, 35, 37, 42-43, 52, 57, 69, 79, 81
; OTHER INFORMATION: a, t, c, g, or other
US-09-294-093B-4883

Query Match 29.1%; Score 23; DB 3; Length 87;
Best Local Similarity 43.7%; Pred. No. 2.2e+02;
Matches 31; Conservative 7; Mismatches 33; Indels 0; Gaps 0;

QY 9 GGGGAGAGACGAGCGGCUUGGCCCCUUAUUGUACUUCGGGCUUGUUGUCUUCUCCUU 68
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Db 73 GGGGAGAGTCGGCTGGNAGTTCCTCATGAAANNCTATNTNGANCTCGCTCGACCTCGCGCA 14
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QY 69 UCGCCACCUCC 79
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 13 ACGTCAGCTCC 3
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

RESULT 3
US-09-849-928-288/c
; Sequence 288, Application US/09849928
; Publication No. US20030059769A1
; GENERAL INFORMATION:
; APPLICANT: PARMA, et al.
; TITLE OF INVENTION: HIGH AFFINITY NUCLEIC ACID LIGANDS
; NUMBER OF SEQUENCES: 390
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Swanson & Bratschun, L.L.C.
; STREET: 8400 E. Prentice Avenue, Suite 200
; CITY: Englewood
; STATE: Colorado
; COUNTRY: USA
; ZIP: 80111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3 1/2 diskette, 1.44 MB
; COMPUTER: IBM pc compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WordPerfect 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/849,928
; FILING DATE: 04-May-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/952,793
; FILING DATE: <Unknown>
; APPLICATION NUMBER: 08/479,724
; FILING DATE: 07-JUNE-1995
; APPLICATION NUMBER: 08/472,256
; FILING DATE: 07-JUNE-1995
; APPLICATION NUMBER: 08/472,255
; FILING DATE: 07-JUNE-1995
; APPLICATION NUMBER: 08/477,829
; FILING DATE: 07-JUNE-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Barry J. Swanson
; REGISTRATION NUMBER: 33,215
; REFERENCE/DOCKET NUMBER: NEX40C/PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (303) 793-3333
; TELEFAX: (303) 793-3433

; INFORMATION FOR SEQ ID NO: 288:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 97 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: RNA
; FEATURE:
; OTHER INFORMATION: All C's are 2'-NH2 cytosine
; FEATURE:
; OTHER INFORMATION: All U's are 2'-NH2 uracil
; SEQUENCE DESCRIPTION: SEQ ID NO: 288:
US-09-849-928-288

Query Match 24.6%; Score 19.4; DB 3; Length 97;
Best Local Similarity 31.1%; Pred. No. 5.1e+03;
Matches 19; Conservative 16; Mismatches 26; Indels 0; Gaps 0;

QY 19 GAGCGGCGUCUGGCCCUUAAUUGUACUUCGGGCGUCGUAUUGUCUUCUCCGCCACCUC 78
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 90 GTGAGCCCTCTGCGAATCTTACTACTTCTGCTTGTGTTTCTTCTTCTGCTGCTCTT 31
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 79 C 79
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 30 C 30
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

RESULT 4
US-10-066-960-288/c
; Sequence 288, Application US/10066960
; Publication No. US20030049644A1
; GENERAL INFORMATION:
; APPLICANT: PARMA, et al.
; TITLE OF INVENTION: HIGH AFFINITY NUCLEIC ACID LIGANDS
; NUMBER OF SEQUENCES: 390
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Swanson & Bratschun, L.L.C.
; STREET: 8400 E. Prentice Avenue, Suite 200
; CITY: Englewood
; STATE: Colorado
; COUNTRY: USA
; ZIP: 80111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3 1/2 diskette, 1.44 MB
; COMPUTER: IBM pc compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WordPerfect 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/066,960
; FILING DATE: 04-Feb-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/952,793
; FILING DATE: 1999-DEC-03
; APPLICATION NUMBER: PCT/US96/09455
; FILING DATE: 05-JUNE-1995
; APPLICATION NUMBER: 08/479,724
; FILING DATE: 07-JUNE-1995
; APPLICATION NUMBER: 08/472,256
; FILING DATE: 07-JUNE-1995
; APPLICATION NUMBER: 08/472,255
; FILING DATE: 07-JUNE-1995
; APPLICATION NUMBER: 08/477,829
; FILING DATE: 07-JUNE-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Barry J. Swanson
; REGISTRATION NUMBER: 33,215
; REFERENCE/DOCKET NUMBER: NEX40C/PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (303) 793-3333
; TELEFAX: (303) 793-3433
; INFORMATION FOR SEQ ID NO: 288:
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SEQUENCE CHARACTERISTICS:
LENGTH: 97 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: RNA
FEATURE:
OTHER INFORMATION: All C's are 2'-NH2 cytosine
FEATURE:
OTHER INFORMATION: All U's are 2'-NH2 uracil
SEQUENCE DESCRIPTION: SEQ ID NO: 288:
US-10-066-960-288

Query Match 24.6%; Score 19.4; DB 6; Length 97;
Best Local Similarity 31.1%; Pred. No. 5.1e+03;
Matches 19; Conservative 16; Mismatches 26; Indels 0; Gaps 0;
QY 19 GAGCGCUCUGCCCUUAUUGUACUUGCGGCGUUAUUGUCUCCUUGCCACCC 78
DB 90 GTGAGCCTCTCTCGAATCTTACTTCTGCTTTGTTTCTTGTGCGTCCCTT 31
QY 79 C 79
DB 30 C 30

RESULT 5
US-10-409-627-288/c
Sequence 288, Application US/10409627
Publication No. US20040043923A1
GENERAL INFORMATION:
APPLICANT: PARMA, et al.
TITLE OF INVENTION: HIGH AFFINITY NUCLEIC ACID LIGANDS
TO LECTINS
NUMBER OF SEQUENCES: 390
CORRESPONDENCE ADDRESS:
ADDRESSEE: Swanson & Bratschun, L.L.C.
STREET: 8400 E. Prentice Avenue, Suite 200
CITY: Englewood
STATE: Colorado
COUNTRY: USA
ZIP: 80111
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3 1/2 diskette, 1.44 MB
COMPUTER: IBM pc compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: WordPerfect 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/409,627
FILING DATE: 07-Apr-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/952,793
FILING DATE: 20-NOVEMBER-1997
APPLICATION NUMBER: PCT/US96/09455
FILING DATE: 05-JUNE-1995
APPLICATION NUMBER: 08/479,724
FILING DATE: 07-JUNE-1995
APPLICATION NUMBER: 08/472,256
FILING DATE: 07-JUNE-1995
APPLICATION NUMBER: 08/472,255
FILING DATE: 07-JUNE-1995
APPLICATION NUMBER: 08/477,829
FILING DATE: 07-JUNE-1995
ATTORNEY/AGENT INFORMATION:
NAME: Barry J. Swanson
REGISTRATION NUMBER: 33,215
REFERENCE/DOCKET NUMBER: NEX40C/PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 793-3333
TELEFAX: (303) 793-3433
INFORMATION FOR SEQ ID NO: 288:
SEQUENCE CHARACTERISTICS:

LENGTH: 97 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: RNA
FEATURE:
OTHER INFORMATION: All C's are 2'-NH2 cytosine
FEATURE:
OTHER INFORMATION: All U's are 2'-NH2 uracil
SEQUENCE DESCRIPTION: SEQ ID NO: 288:
US-10-409-627-288
Query Match 24.6%; Score 19.4; DB 8; Length 97;
Best Local Similarity 31.1%; Pred. No. 5.1e+03;
Matches 19; Conservative 16; Mismatches 26; Indels 0; Gaps 0;
QY 19 GAGCGCUCUGCCCUUAUUGUACUUGCGGCGUUAUUGUCUCCUUGCCACCC 78
DB 90 GTGAGCCTCTCTCGAATCTTACTTCTGCTTTGTTTCTTGTGCGTCCCTT 31
QY 79 C 79
DB 30 C 30
RESULT 6
US-10-705-300-288/c
Sequence 288, Application US/10705300
Publication No. US2004007234A1
GENERAL INFORMATION:
APPLICANT: PARMA, et al.
TITLE OF INVENTION: HIGH AFFINITY NUCLEIC ACID LIGANDS
TO LECTINS
NUMBER OF SEQUENCES: 390
CORRESPONDENCE ADDRESS:
ADDRESSEE: Swanson & Bratschun, L.L.C.
STREET: 8400 E. Prentice Avenue, Suite 200
CITY: Englewood
STATE: Colorado
COUNTRY: USA
ZIP: 80111
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3 1/2 diskette, 1.44 MB
COMPUTER: IBM pc compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: WordPerfect 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/705,300
FILING DATE: 10-Nov-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/952,793
FILING DATE: 20-NOV-1997
APPLICATION NUMBER: PCT/US96/09455
FILING DATE: 05-JUNE-1995
APPLICATION NUMBER: 08/479,724
FILING DATE: 07-JUNE-1995
APPLICATION NUMBER: 08/472,256
FILING DATE: 07-JUNE-1995
APPLICATION NUMBER: 08/472,255
FILING DATE: 07-JUNE-1995
APPLICATION NUMBER: 08/477,829
FILING DATE: 07-JUNE-1995
ATTORNEY/AGENT INFORMATION:
NAME: Barry J. Swanson
REGISTRATION NUMBER: 33,215
REFERENCE/DOCKET NUMBER: NEX40C/PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 793-3333
TELEFAX: (303) 793-3433
INFORMATION FOR SEQ ID NO: 288:
SEQUENCE CHARACTERISTICS:
LENGTH: 97 base pairs

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; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: RNA
; FEATURE:
; OTHER INFORMATION: All C's are 2'-NH2 cytosine
; FEATURE:
; OTHER INFORMATION: All U's are 2'-NH2 uracil
; SEQUENCE DESCRIPTION: SEQ ID NO: 288:
US-10-705-300-288

Query Match      24.6%; Score 19.4; DB 8; Length 97;
Best Local Similarity 31.1%; Pred. No. 5.1e+03;
Matches 19; Conservative 16; Mismatches 26; Indels 0; Gaps 0;

QY 19 GAGCGGCGUGGCCCCUUAUUGUACUUGCGGCGUGUUGUCUCCUUUGCCACUUC 78
Db 90 GTGAGCTCTGTCGAATCTTACTACTTCTGCTTGTGTTTGTGTTTGTGCTGCTT 31
QY 79 C 79
Db 30 C 30

RESULT 7
US-10-448-250-6
; Sequence 6, Application US/10448250
; Publication No. US20040018530A1
; GENERAL INFORMATION:
; APPLICANT: Bowser, Michael T
; APPLICANT: Mendonsa, Shaun D
; TITLE OF INVENTION: IN VITRO EVOLUTION OF FUNCTIONAL RNA AND DNA USING
; TITLE OF INVENTION: ELECTROPHORETIC SELECTION
; FILE REFERENCE: 110.01870101
; CURRENT APPLICATION NUMBER: US/10/448,250
; PRIOR FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: 60/384,709
; PRIOR FILING DATE: 2002-05-31
; PRIOR APPLICATION NUMBER: 60/470,750
; PRIOR FILING DATE: 2003-05-15
; NUMBER OF SEQ ID NOS: 127
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 6
; LENGTH: 80
; TYPE: DNA
; ORGANISM: ARTIFICIAL SEQUENCE
; FEATURE:
; OTHER INFORMATION: aptamer
US-10-448-250-6

Query Match      24.3%; Score 19.2; DB 8; Length 80;
Best Local Similarity 35.9%; Pred. No. 5.9e+03;
Matches 23; Conservative 13; Mismatches 28; Indels 0; Gaps 0;

QY 6 GCGGCGGAGAGACGCGGCGUCUUGCGGCCCCUUAUUGUACUUGCGGCGUGUUGUCUCUC 65
Db 2 GCAGCAGAGGTCAGATGTTGTACCGTTATTTGTGCTAGCATCCCCGGGTAC 61
QY 66 CUU 69
Db 62 CTAT 65

RESULT 8
US-09-983-965-1387
; Sequence 1387, Application US/09983965
; Patent No. US20020137160A1
; GENERAL INFORMATION:
; APPLICANT: Warren, Wesley C.
; APPLICANT: Rao, Nengping
; APPLICANT: Byatt, John C.
; APPLICANT: Mathialagan, Nagappan
; TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
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; TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION
; FILE REFERENCE: 37-21(10297)C
; CURRENT APPLICATION NUMBER: US/09/983,965
; CURRENT FILING DATE: 2001-10-26
; PRIOR APPLICATION NUMBER: US 09/465,231
; PRIOR FILING DATE: 1999-12-15
; PRIOR APPLICATION NUMBER: US 60/113,678
; PRIOR FILING DATE: 1998-12-17
; NUMBER OF SEQ ID NOS: 5912
; SEQ ID NO 1387
; LENGTH: 87
; TYPE: DNA
; ORGANISM: Bos taurus
; FEATURE:
; OTHER INFORMATION: Clone ID: 23-LIB2809-008-Q1-E1-F3
US-09-983-965-1387

Query Match      24.3%; Score 19.2; DB 3; Length 87;
Best Local Similarity 37.5%; Pred. No. 5.9e+03;
Matches 15; Conservative 12; Mismatches 13; Indels 0; Gaps 0;

QY 31 CCCUUAUUGUACUUGCGGCGUCGUUUGUCUUCUUCUUC 70
Db 39 CCTCTTAATCTATATCTTACTCCAATTCACCTCCCTCTC 78

RESULT 9
US-11-106-909-22
; Sequence 22, Application US/11106909
; Publication No. US20060029950A1
; GENERAL INFORMATION:
; APPLICANT: WHITTEN, Jeffrey P.
; APPLICANT: SCHWABER, Michael
; APPLICANT: SIDDIQUI-JAIN, Adam
; APPLICANT: MORAN, Terence
; TITLE OF INVENTION: SUBSTITUTED QUINOBENZOXAZINE ANALOGS AND
; TITLE OF INVENTION: METHODS OF USING THEREOF
; FILE REFERENCE: 532232001121
; CURRENT APPLICATION NUMBER: US/11/106,909
; CURRENT FILING DATE: 2005-04-15
; PRIOR APPLICATION NUMBER: US 10/903,975
; PRIOR FILING DATE: 2004-07-30
; PRIOR APPLICATION NUMBER: US 10/821,243
; PRIOR FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/461,271
; PRIOR FILING DATE: 2004-07-03
; PRIOR APPLICATION NUMBER: US 60/463,171
; PRIOR FILING DATE: 2003-04-15
; PRIOR APPLICATION NUMBER: US 60/519,535
; PRIOR FILING DATE: 2003-11-12
; PRIOR APPLICATION NUMBER: US 60/532,727
; PRIOR FILING DATE: 2003-12-23
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 22
; LENGTH: 86
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-106-909-22

Query Match      24.1%; Score 19; DB 16; Length 86;
Best Local Similarity 42.4%; Pred. No. 7.1e+03;
Matches 25; Conservative 9; Mismatches 25; Indels 0; Gaps 0;

QY 4 GGGCGGGGAGACGAGCGGCGUCUGGCCCCUUAUUGUACUUGCGGCGUGUUGUCU 62
Db 9 GGGCGGGGCGGGCGGGGCTTAGCGACACCAATTTCTATAGTCGTTAGCT 67

RESULT 10
US-11-228-636-22
; Sequence 22, Application US/11228636
; Publication No. US20060074089A1
```


GENERAL INFORMATION:
APPLICANT: WHITTEN, Jeffrey P.
APPLICANT: PIERRE, Fabrice
APPLICANT: REGAN, Collin
APPLICANT: SCHWABE, Michael
APPLICANT: YIANNIKOUDOS, George Petros
APPLICANT: JUNG, Michael
APPLICANT: NAGASAWA, Johnny Y.
APPLICANT: CHUA, Peter
TITLE OF INVENTION: QUINOLONE ANALOGS
FILE REFERENCE: 532232001820
CURRENT APPLICATION NUMBER: US/11/228,636
CURRENT FILING DATE: 2005-09-16
PRIOR APPLICATION NUMBER: US 11/149,007
PRIOR FILING DATE: 2005-06-09
PRIOR APPLICATION NUMBER: US 60/611,030
PRIOR FILING DATE: 2004-09-17
PRIOR APPLICATION NUMBER: US 60/638,603
PRIOR FILING DATE: 2004-12-22
PRIOR APPLICATION NUMBER: US 60/688,986
PRIOR FILING DATE: 2005-06-09
PRIOR APPLICATION NUMBER: US 60/688,796
PRIOR FILING DATE: 2005-06-09
NUMBER OF SEQ ID NOS: 29
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 22
LENGTH: 86
TYPE: DNA
ORGANISM: Homo sapiens
US-11-228-636-22

Query Match 24.1%; Score 19; DB 16; Length 86;
Best Local Similarity 42.4%; Pred. No. 7.1e+03;
Matches 25; Conservative 9; Mismatches 25; Indels 0; Gaps 0;
QY 4 GGGCGGGGAGACGACGAGCGGCGUCGCGCCCUAAUUGUACUCGCGGCGUUAUUCU 62
DB 9 GGGCGGGGCGGGCGGGGGGCTTAGCCACACGCAATTCGTATAGTGAGTCGTATTAGCT 67

RESULT 11
US-10-310-914A-37212/c
Sequence 37212, Application US/10310914A
Publication No. US20060003322A1
GENERAL INFORMATION:
APPLICANT: Bentwich, Isaac
APPLICANT: Shiler, Knizat
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
FILE REFERENCE: 06087.0200.CPUS01
CURRENT APPLICATION NUMBER: US/10/310,914A
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: PatentIn version 3.3
SEQ ID NO 37212
LENGTH: 24
TYPE: RNA
ORGANISM: Human
US-10-310-914A-37212

Query Match 23.8%; Score 18.8; DB 11; Length 24;
Best Local Similarity 90.9%; Pred. No. 7.1e+03;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 GGAGGGCGGGGAGACGAGC 22
DB 24 GGAGGGCTGGGAGAGAGC 3

RESULT 12
US-10-407-123-19
Sequence 19, Application US/10407123
Publication No. US20030181381A1

GENERAL INFORMATION:
APPLICANT: Himmelspach, Michele
APPLICANT: Schlokot, Uwe
APPLICANT: Dörner, Friedrich
APPLICANT: Fisch, Andreas
APPLICANT: Eibl, Johann
TITLE OF INVENTION: Factor X Analogues With
a Modified Protease Cleavage Site
NUMBER OF SEQUENCES: 122
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: CA
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/407,123
FILING DATE: 04-Apr-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/367,791A
FILING DATE: 12-No. US20030181381A1-1999
APPLICATION NUMBER: AT A 335/97
FILING DATE: 27-FEB-1997
APPLICATION NUMBER: WO PCT/AT98/00045
FILING DATE: 27-FEB-1998
ATTORNEY/AGENT INFORMATION:
NAME: Ausehus, Scott L.
REGISTRATION NUMBER: 42,471
REFERENCE/DOCKET NUMBER: 20695D-000700US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 39 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
SEQUENCE DESCRIPTION: SEQ ID NO: 19:
US-10-407-123-19

Query Match 23.8%; Score 18.8; DB 7; Length 39;
Best Local Similarity 44.7%; Pred. No. 7.6e+03;
Matches 17; Conservative 9; Mismatches 12; Indels 0; Gaps 0;
QY 33 CCUUAUUGUACUCGCGGCGUUAUUGUCUCCUUUC 70
DB 2 CCAGAATCGATTCTGCTGCTGTGTGCGCCCTCTC 39

RESULT 13
US-09-918-740-15/c
Sequence 15, Application US/09918740
Publication No. US20030033626A1
GENERAL INFORMATION:
APPLICANT: Hahn, Frederick
APPLICANT: Kuehnle, Adelheid
TITLE OF INVENTION: Manipulation of genes of the mevalonate and isoprenoid pathways t
FILE REFERENCE: KAS-103XC1
CURRENT APPLICATION NUMBER: US/09/918,740
CURRENT FILING DATE: 2001-07-31
PRIOR APPLICATION NUMBER: 60/221,703
PRIOR FILING DATE: 2000-07-31

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OM nucleic - nucleic search, using sw model

Run on: October 16, 2006, 14:34:29 ; Search time 139 Seconds
(without alignments)
1061.937 Million cell updates/sec

Title: US-10-604-726A-5135
Perfect score: 79
Sequence: 1 ggaaggcggggagagacga.....ucuccuunegccaccucc 79

Scoring table: IDENTITY NUC
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Searched: 2395520 seqs, 934235491 residues

Total number of hits satisfying chosen parameters: 3222406

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US06_NEW_PUB.seq.*
3: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US07_NEW_PUB.seq.*
4: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US08_NEW_PUB.seq.*
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9: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11_NEW_PUB.seq.*
10: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US60_NEW_PUB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	18.6	23.5	99	8	US-11-217-529-173876 Sequence 173876,
2	18.4	23.3	51	8	US-11-143-642-1090 Sequence 1090, Ap
3	18.2	23.0	50	6	US-10-554-711-648 Sequence 648, App
4	18.2	23.0	50	6	US-10-554-759-648 Sequence 648, App
5	17.8	22.5	77	7	US-11-357-615-25 Sequence 25, Appli
6	17.8	22.5	90	6	US-10-526-765-9 Sequence 9, Appli
7	17.2	21.8	25	9	US-11-348-413-618728 Sequence 618728,
8	17.2	21.8	66	9	US-11-375-551-85 Sequence 85, Appl
9	17.2	21.8	76	7	US-11-374-388-403 Sequence 403, App
10	17.2	21.8	99	6	US-10-531-545-10 Sequence 10, Appli
11	17	21.5	25	9	US-11-348-413-216548 Sequence 216548,
12	17	21.5	47	7	US-11-370-584-3264 Sequence 3264, Ap
13	17	21.5	93	8	US-11-243-296A-5 Sequence 5, Appli
14	16.6	21.0	25	9	US-11-348-413-216546 Sequence 216546,
15	16.6	21.0	25	9	US-11-348-413-216547 Sequence 216547,
16	16.6	21.0	80	9	US-11-267-769-77 Sequence 77, Appl
17	16.6	21.0	80	9	US-11-267-807-77 Sequence 77, Appl
18	16.6	21.0	90	7	US-11-280-456-20 Sequence 20, Appl
19	16.4	20.8	93	9	US-11-348-413-8848 Sequence 8848, Ap
20	16.4	20.8	93	9	US-11-348-413-9715 Sequence 9715, Ap
21	16.2	20.5	25	8	US-11-217-529-34950 Sequence 34950, A
22	16.2	20.5	25	9	US-11-348-413-425880 Sequence 425880,
23	16.2	20.5	25	9	US-11-348-413-425881 Sequence 425881,

ALIGNMENTS

RESULT 1
US-11-217-529-173876
; Sequence 173876, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 173876
; LENGTH: 99
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-173876
Query Match 23.5%; Score 18.6; DB 8; Length 99;
Best Local Similarity 39.4%; Pred. No. 2e+03; 9; Indels 0; Gaps 0;
Matches 13; Conservative 11; Mismatches 9; Indels 0; Gaps 0;
QY 39 UUGUACUUGGGGUGUAUUGUCUUCUUCG 71
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Db 39 TTGTTGGTCGGGCTGCTTGGACCCATTTCG 71
RESULT 2
US-11-143-642-1090
; Sequence 1090, Application US/11143642
; Publication No. US20060099610A1
; GENERAL INFORMATION:
; APPLICANT: Jukka T. SALONEN et al.
; TITLE OF INVENTION: METHOD AND KIT FOR DETECTING A RISK OF ACUTE MYOCARDIAL INFARCTION
; FILE REFERENCE: 0933-0245FUS1
; CURRENT APPLICATION NUMBER: US/11/143,642
; CURRENT FILING DATE: 2005-06-03
; NUMBER OF SEQ ID NOS: 2039
; SOFTWARE: PatentIn version 3.3

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Sequence 425883,
Sequence 425884,
Sequence 425884,
Sequence 1066900,
Sequence 216549,
Sequence 998589,
Sequence 13457, A
Sequence 5433, Ap
Sequence 5433, Ap
Sequence 5433, Ap
Sequence 49, Appl
Sequence 32, Appl
Sequence 194, App
Sequence 511518,
Sequence 546599,
Sequence 638059,
Sequence 1162729,
Sequence 1162730,
Sequence 1162731,
Sequence 1207851,
Sequence 1207852,

24 16.2 20.5 25 9 US-11-348-413-425882
25 16.2 20.5 25 9 US-11-348-413-425883
26 16.2 20.5 25 9 US-11-348-413-425884
27 16.2 20.5 25 9 US-11-348-413-1066900
C 28 16 20.3 25 9 US-11-348-413-216549
C 29 16 20.3 25 9 US-11-348-413-998589
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C 32 16 20.3 96 7 US-11-434-184-5433
C 33 16 20.3 96 7 US-11-434-199-5433
C 34 16 20.3 96 7 US-11-434-203-5433
C 35 15.8 20.0 87 8 US-11-213-668-49
C 36 15.8 20.0 93 8 US-11-213-668-32
C 37 15.8 20.0 99 7 US-11-043-824-194
C 38 15.6 19.7 25 9 US-11-348-413-511518
C 39 15.6 19.7 25 9 US-11-348-413-546599
C 40 15.6 19.7 25 9 US-11-348-413-638059
C 41 15.6 19.7 25 9 US-11-348-413-1162729
C 42 15.6 19.7 25 9 US-11-348-413-1162730
C 43 15.6 19.7 25 9 US-11-348-413-1162731
C 44 15.6 19.7 25 9 US-11-348-413-1207851
C 45 15.6 19.7 25 9 US-11-348-413-1207852

; SEQ ID NO 1090
; LENGTH: 51
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-11-143-642-1090

Query Match 23.3%; Score 18.4; DB 8; Length 51;
Best Local Similarity 41.3%; Pred. No. 2e+03;
Matches 19; Conservative 10; Mismatches 17; Indels 0; Gaps 0;

QY 32 CCCTAAATATCTCGGCGAGTAYCGTAAATCTCTGTCCTC 46
Db 1 CCCTAAATATCTCGGCGAGTAYCGTAAATCTCTGTCCTC 46

RESULT 3

US-10-554-711-648
; Sequence 648, Application US/10554711
; Publication No. US20060115806A1
; GENERAL INFORMATION:
; APPLICANT: University of Georgia Research Foundation
; APPLICANT: McDonald, John F.
; TITLE OF INVENTION: Global Analysis of Transposable Elements
; FILE REFERENCE: 21099.0075P1
; CURRENT APPLICATION NUMBER: US/10/554,711
; CURRENT FILING DATE: 2005-10-28
; PRIOR APPLICATION NUMBER: 60/466,798
; PRIOR FILING DATE: 2003-04-29
; NUMBER OF SEQ ID NOS: 778
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 648
; LENGTH: 50
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:/note =
; OTHER INFORMATION: Synthetic Construct
US-10-554-711-648

Query Match 23.0%; Score 18.2; DB 6; Length 50;
Best Local Similarity 48.4%; Pred. No. 2.4e+03;
Matches 15; Conservative 8; Mismatches 8; Indels 0; Gaps 0;

QY 45 UUCGGCUCGUUUGUCUCUCCUUGCGCCAC 75
Db 12 TTGGGACTCGGACTGCTCTTGTCTCTC 42

RESULT 4

US-10-554-759-648
; Sequence 648, Application US/10554759
; Publication No. US20060177825A1
; GENERAL INFORMATION:
; APPLICANT: University of Georgia Research Foundation
; APPLICANT: McDonald, John F.
; TITLE OF INVENTION: Global Analysis of Transposable Elements
; FILE REFERENCE: 21099.0077P1
; CURRENT APPLICATION NUMBER: US/10/554,759
; CURRENT FILING DATE: 2005-10-28
; PRIOR APPLICATION NUMBER: 60/466,801
; PRIOR FILING DATE: 2003-04-29
; NUMBER OF SEQ ID NOS: 770
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 648
; LENGTH: 50
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:/note =
; OTHER INFORMATION: Synthetic Construct

US-10-554-759-648

Query Match 23.0%; Score 18.2; DB 6; Length 50;
Best Local Similarity 48.4%; Pred. No. 2.4e+03;
Matches 15; Conservative 8; Mismatches 8; Indels 0; Gaps 0;

QY 45 UUCGGCUCGUUUGUCUCUCCUUGCGCCAC 75
Db 12 TTGGGACTCGGACTGCTCTTGTCTCTC 42

RESULT 5

US-11-357-615-25
; Sequence 25, Application US/11357615
; Publication No. US20060188972A1
; GENERAL INFORMATION:
; APPLICANT: WOLFFE, Alan P.
; APPLICANT: COLLINGWOOD, Trevor
; TITLE OF INVENTION: TARGETED MODIFICATION OF CHROMATIN STRUCTURE
; FILE REFERENCE: 8325-0014 / S14-US1
; CURRENT APPLICATION NUMBER: US/11/357,615
; CURRENT FILING DATE: 2006-02-16
; PRIOR APPLICATION NUMBER: US/09/844,508
; PRIOR FILING DATE: 2001-04-27
; PRIOR APPLICATION NUMBER: 60/200,590
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: 60/228,523
; PRIOR FILING DATE: 2000-08-28
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 25
; LENGTH: 77
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: fragment
; OTHER INFORMATION: encoding DGGGS linker, 3' to 5'
US-11-357-615-25

Query Match 22.5%; Score 17.8; DB 7; Length 77;
Best Local Similarity 37.8%; Pred. No. 3.8e+03;
Matches 14; Conservative 11; Mismatches 12; Indels 0; Gaps 0;

QY 40 UGUACUUGCGGUCGUUUGUCUCUCCUUGCGCCACC 76
Db 3 TGTATTGTGGTGCTGTGTTCTTCTGCCGCCACC 39

RESULT 6

US-10-526-765-9/c
; Sequence 9, Application US/10526765
; Publication No. US20060121049A1
; GENERAL INFORMATION:
; APPLICANT: LETOURNEUR, Odile
; TITLE OF INVENTION: CHIMERIC RECOMBINANT PROTEIN AND IN VITRO DIAGNOSIS
; FILE REFERENCE: 122802
; CURRENT APPLICATION NUMBER: US/10/526,765
; CURRENT FILING DATE: 2005-03-07
; PRIOR APPLICATION NUMBER: PCT/FR03/02712
; PRIOR FILING DATE: 2003-09-15
; PRIOR APPLICATION NUMBER: FR 02/11485
; PRIOR FILING DATE: 2002-09-17
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 9
; LENGTH: 90
; TYPE: DNA
; ORGANISM: Human immunodeficiency virus type 1
US-10-526-765-9

Query Match 22.5%; Score 17.8; DB 6; Length 90;
Best Local Similarity 35.6%; Pred. No. 3.9e+03;
Matches 16; Conservative 12; Mismatches 17; Indels 0; Gaps 0;

```
QY 35 UUAUUGUACUUGGGGCUUUAUUGUCUUCUCCUCCUCCUCCUCC 79
      |||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db 45 TTTATATAATTCACTTCTCCAAATGTCCTCATATCTCTCTCTCC 1

RESULT 7
US-11-348-413-618728/c
; Sequence 618728, Application US/11348413
; Publication No. US20060160121A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; APPLICANT: Murphy, Ellen
; APPLICANT: Olmsted, Stephen
; TITLE OF INVENTION: PROBE ARRAYS FOR DETECTING MULTIPLE STRAINS OF DIFFERENT SPECIES
; FILE REFERENCE: 031896-084100 (AM 101724)
; CURRENT APPLICATION NUMBER: US/11/348,413
; CURRENT FILING DATE: 2006-02-07
; PRIOR APPLICATION NUMBER: PCT/US05/035471
; PRIOR FILING DATE: 2005-10-05
; PRIOR APPLICATION NUMBER: US 11/243,445
; PRIOR FILING DATE: 2005-10-05
; PRIOR APPLICATION NUMBER: US 60/615,573
; PRIOR FILING DATE: 2004-10-05
; NUMBER OF SEQ ID NOS: 1276209
; SEQ ID NO 618728
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)-(25)
; OTHER INFORMATION: SEQ ID NO: 370; WAN01UUA4-5_at; Start 75; Stop 99;
; OTHER INFORMATION: 01101100000000
US-11-348-413-618728

Query Match 21.8%; Score 17.2; DB 9; Length 25;
Best Local Similarity 40.9%; Pred. No. 4.5e+03;
Matches 9; Conservative 10; Mismatches 3; Indels 0; Gaps 0;

QY 50 GCUCGUUUGUCUCUCCUUCG 71
      |||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db 25 GGTGCTATTCTCTCATTTGC 4

RESULT 8
US-11-375-551-85
; Sequence 85, Application US/11375551
; Publication No. US20060156434A1
; GENERAL INFORMATION:
; APPLICANT: Bintrim, Scott
; APPLICANT: Mitchell, Jon
; APPLICANT: Larrinua, Ignacio
; APPLICANT: Apel-Birkhold, Patricia
; APPLICANT: Schafer, Barry
; APPLICANT: Bevan, Scott
; APPLICANT: Young, Scott
; APPLICANT: Guo, Lining
; TITLE OF INVENTION: Xenorhabdus TC Proteins and Genes for Pest Control
; FILE REFERENCE: DAS-105X
; CURRENT APPLICATION NUMBER: US/11/375,551
; CURRENT FILING DATE: 2006-03-14
; PRIOR APPLICATION NUMBER: US/10/753,901
; PRIOR FILING DATE: 2004-01-07
; PRIOR APPLICATION NUMBER: US 60/441,717
; PRIOR FILING DATE: 2003-01-21
; NUMBER OF SEQ ID NOS: 85
; SOFTWARE: Patentin version 3.3
; SEQ ID NO 85
; LENGTH: 66
```

```
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Reverse primer sequence used to amplify xptB1
US-11-375-551-85

Query Match 21.8%; Score 17.2; DB 9; Length 66;
Best Local Similarity 36.8%; Pred. No. 6e+03;
Matches 14; Conservative 11; Mismatches 13; Indels 0; Gaps 0;

QY 24 GCUCUGGCCUUAUUGUACUUCGGGCUUGUUGUC 61
      |||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db 1 GCTCGAGCAGATTATTATGCTTCGGATTCATTATGAC 38

RESULT 9
US-11-374-388-403
; Sequence 403, Application US/11374388
; Publication No. US20060193870A1
; GENERAL INFORMATION:
; APPLICANT: King, Gordon E.
; APPLICANT: Meagher, Madeleine Joy
; APPLICANT: Xu, Jiangchun
; APPLICANT: Secrist, Heather
; APPLICANT: Jiang, Yugu
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF COLON CANCER
; FILE REFERENCE: 210121.547C6
; CURRENT APPLICATION NUMBER: US/11/374,388
; CURRENT FILING DATE: 2006-03-13
; PRIOR APPLICATION NUMBER: US 10/099,926
; PRIOR FILING DATE: 2002-03-14
; PRIOR APPLICATION NUMBER: US 10/033,528
; PRIOR FILING DATE: 2001-12-26
; PRIOR APPLICATION NUMBER: US 09/920,300
; PRIOR FILING DATE: 2001-07-31
; PRIOR APPLICATION NUMBER: US 60/302,051
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 60/279,763
; PRIOR FILING DATE: 2001-03-28
; PRIOR APPLICATION NUMBER: US 60/223,283
; PRIOR FILING DATE: 2000-08-03
; NUMBER OF SEQ ID NOS: 1982
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 403
; LENGTH: 76
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 7, 11, 18, 30, 31, 46, 47, 61, 62
; OTHER INFORMATION: n = A,T,C or G
US-11-374-388-403

Query Match 21.8%; Score 17.2; DB 7; Length 76;
Best Local Similarity 51.4%; Pred. No. 6.3e+03;
Matches 18; Conservative 4; Mismatches 13; Indels 0; Gaps 0;

QY 7 CGGGGAGACGAGCGGCUUGCCUCCUUAUUG 41
      |||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db 1 CTGGGANATGNCAGCTCTCTGGCATCTNNATGG 35

RESULT 10
US-10-531-545-10
; Sequence 10, Application US/10531545
; Publication No. US20060183106A1
; GENERAL INFORMATION:
; APPLICANT: SIDDQUI-JAIN, Adam
; TITLE OF INVENTION: PROCESSES FOR IDENTIFYING
; TITLE OF INVENTION: QUADRUPLIX-TARGETED ANTIVIRAL MOLECULES
; FILE REFERENCE: 532232000900
; CURRENT APPLICATION NUMBER: US/10/531,545
```



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US-11-348-413-216546/c
; Sequence 216546, Application US/11348413
; Publication No. US20060160121A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; APPLICANT: Murphy, Ellen
; APPLICANT: Olmsted, Stephen
; TITLE OF INVENTION: PROBE ARRAYS FOR DETECTING MULTIPLE STRAINS OF DIFFERENT SPECIES
; FILE REFERENCE: 031896-084100 (AM 101724)
; CURRENT APPLICATION NUMBER: US/11/348,413
; CURRENT FILING DATE: 2006-02-07
; PRIOR APPLICATION NUMBER: PCT/US05/035471
; PRIOR FILING DATE: 2005-10-05
; PRIOR APPLICATION NUMBER: US 11/243,445
; PRIOR FILING DATE: 2005-10-05
; PRIOR APPLICATION NUMBER: US 60/615,573
; PRIOR FILING DATE: 2004-10-05
; NUMBER OF SEQ ID NOS: 1276209
; SEQ ID NO 216546
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: probe
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(25)
; OTHER INFORMATION: SEQ ID NO: 6358; WAN01UKNQ; Start 1513; Stop 1537;
; OTHER INFORMATION: 00000001100000
; US-11-348-413-216546

```

Query Match 21.0%; Score 16.6; DB 9; Length 25;
Best Local Similarity 39.1%; Pred. No. 7.5e+03;
Matches 9; Conservative 10; Mismatches 4; Indels 0; Gaps 0;

Qy 38 AUUGUACUUCGGGCUCGUAUUGU 60
|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:
pb 25 ATTGTAATTCGGATGGTATTGT 3

RESULT 15
US-11-348-413-216547/c
; Sequence 216547, Application US/11348413
; Publication No. US20060160121A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; APPLICANT: Murphy, Ellen
; APPLICANT: Olmsted, Stephen
; TITLE OF INVENTION: PROBE ARRAYS FOR DETECTING MULTIPLE STRAINS OF DIFFERENT SPECIES
; FILE REFERENCE: 031896-084100 (AM 101724)
; CURRENT APPLICATION NUMBER: US/11/348,413
; CURRENT FILING DATE: 2006-02-07
; PRIOR APPLICATION NUMBER: PCT/US05/035471
; PRIOR FILING DATE: 2005-10-05
; PRIOR APPLICATION NUMBER: US 11/243,445
; PRIOR FILING DATE: 2005-10-05
; PRIOR APPLICATION NUMBER: US 60/615,573
; PRIOR FILING DATE: 2004-10-05
; NUMBER OF SEQ ID NOS: 1276209
; SEQ ID NO 216547
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: probe
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(25)
; OTHER INFORMATION: SEQ ID NO: 6358; WANO1UKNQ; Start 1514; Stop 1538;
; OTHER INFORMATION: 00000001100000
US-11-348-413-216547

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GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 16, 2006, 13:53:09 ; Search time 125.594 Seconds
(without alignments)
1332.341 Million cell updates/sec

Title: US-10-604-726A-5136
Perfect score: 24
Sequence: 1 uauugucucuccuucgccaccuc 24

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 5244920 seqs, 3486124231 residues

Total number of hits satisfying chosen parameters: 4443654

Minimum DB seq length: 0
Maximum DB seq length: 30

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_8.*
1: Geneseqn1980s:*
2: Geneseqn1990s:*
3: Geneseqn2000s:*
4: Geneseqn2001as:*
5: Geneseqn2001bs:*
6: Geneseqn2002as:*
7: Geneseqn2002bs:*
8: Geneseqn2003as:*
9: Geneseqn2003bs:*
10: Geneseqn2003cs:*
11: Geneseqn2003ds:*
12: Geneseqn2004as:*
13: Geneseqn2004bs:*
14: Geneseqn2005s:*
15: Geneseqn2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	15.8	65.8	24	4	AAD21686
C 2	15.6	65.0	24	2	AAQ44801
C 3	15.6	65.0	24	2	AAQ44806
C 4	15.6	65.0	24	2	AAT99274
C 5	15.6	65.0	24	2	AAV31726
C 6	15.6	65.0	24	2	AAV31731
C 7	15.6	65.0	24	2	AAQ4070
C 8	15.6	65.0	24	2	AAQ4075
C 9	15.6	65.0	25	15	AE94315
C 10	15.2	63.3	21	7	ADI94591
C 11	15.2	63.3	22	7	ADI94589
C 12	15.2	63.3	27	7	ADI94590
C 13	15.2	63.3	28	7	ADI94588
C 14	14.8	61.7	29	2	AAV91451
C 15	14.8	61.7	29	3	AAF01081
C 16	14.6	60.8	30	14	ADX99968
C 17	14.4	60.0	18	2	AAQ5826
C 18	14.4	60.0	20	7	ADI94593

C 19	14.4	60.0	23	2	AAQ85989
C 20	14.4	60.0	26	7	ADI94592
C 21	14.2	59.2	21	2	AAQ56946
C 22	14.2	59.2	21	15	AEF13105
C 23	14.2	59.2	25	10	ADC05103
C 24	14.2	59.2	25	10	ADC05104
C 25	14.2	59.2	25	10	ADC05109
C 26	14.2	59.2	25	10	ADC05105
C 27	14.2	59.2	25	10	ADC05108
C 28	14.2	59.2	25	10	ADC05106
C 29	14.2	59.2	25	10	ADC05107
C 30	14	58.3	24	2	AAQ38850
C 31	14	58.3	24	2	AAQ44802
C 32	14	58.3	24	2	AAV99270
C 33	14	58.3	24	2	AAV31727
C 34	14	58.3	24	2	AAQ4071
C 35	14	58.3	24	5	AAH48099
C 36	14	58.3	24	14	ASC26021
C 37	14	58.3	24	14	ABC28387
C 38	14	58.3	25	9	ACK16088
C 39	14	58.3	30	8	ACD27983
C 40	14	58.3	30	10	ADA09553
C 41	13.8	57.5	17	10	ADC03597
C 42	13.8	57.5	20	2	AAQ94034
C 43	13.8	57.5	20	8	ABX04519
C 44	13.8	57.5	20	10	ADC01938
C 45	13.8	57.5	20	10	AAQ59884

ALIGNMENTS

RESULT 1
AAD21686/c
ID AAD21686 standard; DNA; 24 BP.
XX AAD21686;

28-JAN-2002 (first entry)

Imperfect direct repeat #1 of human RPGR exon ORF15 repetitive sequence.
Human; mutation; retinitis pigmentosa GTPase regulator; RPGR; genotyping;
open reading frame; ORF; X-linked retinitis pigmentosa; XLRP;
gene therapy; screening; forensic analysis; ds.
Homo sapiens.
WO200177380-A2.
18-OCT-2001.
10-APR-2001; 2001WO-GB001622.
10-APR-2000; 2000GB-00008801.
(MEDI-) MEDICAL RES COUNCIL.
Wright A;
WPI; 2001-663057/76.

Diagnosing disease or predisposition to disease, associated with disease causing mutations in retinitis pigmentosa GTPase regulator gene by genotyping ORF15 of the gene, and determining presence of mutations.

Disclosure; Fig 4E, 100pp; English.

The present invention relates to a method for diagnosing disease or predisposition to a disease, associated with a disease causing mutations in a retinitis pigmentosa GTPase regulator (RPGR) gene involves genotyping a RPGR gene, and determining whether the genotype comprises a disease causing mutations, where the risk genotype is present within open

CC reading frame (ORF)15 of the RPGR gene. The method is useful for
CC detecting a certain disease state e.g., X-linked retinitis pigmentosa
CC (XLRP). The kit is useful for detecting and measuring disease causing
CC mutations in biological fluids and tissues and for localising mutation in
CC tissues. The mutant RPGR gene is useful in gene therapy techniques and
CC for screening agents capable of affecting the expression of the sequences
CC and/or the biological activity of mutant RPGR. They are preferably useful
CC for identifying agonists and antagonists of RPGR. The mutant RPGR gene is
CC also useful in identification of potential pharmaceutical targets in high
CC throughput screening assays and forensic analysis. The present sequence
CC is the imperfect direct repeat of human RPGR exon ORF15 repetitive DNA
XX
SQ Sequence 24 BP; 10 A; 0 C; 14 G; 0 T; 0 U; 0 Other;

Query Match 65.8%; Score 15.8; DB 4; Length 24;
Best Local Similarity 52.6%; Pred. No. 3.7e+03;
Matches 10; Conservative 7; Mismatches 2; Indels 0; Gaps 0;

QY 6 UCUCUCUUCGCCACCUC 24
Db 19 TCCTCTCTCTCCCTCTCTC 1

RESULT 2
AAQ44801/c
ID AAQ44801 standard; DNA; 24 BP.

XX AC AAQ44801;

XX DT 25-MAR-2003 (revised)
DT 28-SEP-1994 (first entry)

XX DE Purine-rich PUR element.

XX Single-strand binding protein; PUR protein; cellular oncogene;
XX eukaryotic origin of replication; gene amplification; cancer cell;
KW retinoblastoma protein; helix-destabilising protein; inhibitor;
KW hyperproliferation; ss.

XX OS Homo sapiens.

XX PN WO9405689-A1.

XX PD 17-MAR-1994.

XX PF 27-AUG-1993; 93WO-US008102.

XX PR 28-AUG-1992; 92US-00938189.

XX PR 02-FEB-1993; 93US-00014943.

XX PA (MOUN) MOUNT SINAI SCHOOL MEDICINE.

XX PI Johnson EM, Bergemann AD;

XX PI WPI; 1994-101114/12.

XX Cloning and expression of PUR protein, involved in regulation of DNA
PT replication - also oligo:nucleotide(s) and antibodies for use in the
PT treatment of proliferative diseases, e.g. cancer.

XX PS Claim 6; Page 65; 97pp; English.

XX PUR elements are purine-rich 24 nucleotide DNA sequences which occur at
CC eukaryotic origins of replication and 5' flanking regions of some
CC cellular oncogenes. The PUR protein (AAR50310) was originally identified
CC as a 27kD HeLa cell nuclear factor that bound in a sequence-specific
CC manner to a major site of DNA bending located 1.6kb upstream of the
CC transcription start site of the human c-myc gene; the site recognised by
CC PUR protein had the sequence AAQ44801. (Updated on 25-MAR-2003 to correct
CC PN field.)

XX SQ Sequence 24 BP; 8 A; 0 C; 14 G; 2 T; 0 U; 0 Other;

Query Match 65.0%; Score 15.6; DB 2; Length 24;
Best Local Similarity 50.0%; Pred. No. 4.5e+03;
Matches 11; Conservative 7; Mismatches 4; Indels 0; Gaps 0;

QY 3 UUGUCUCUUCGCCACCUC 24
Db 23 TTTTCTCTCTCCCTCCACCCTC 2

RESULT 3
AAQ44806
ID AAQ44806 standard; DNA; 24 BP.

XX AC AAQ44806;

XX DT 25-MAR-2003 (revised)
DT 28-SEP-1994 (first entry)

XX DE Oligonucleotide MR0700 used in characterising c-myc PUR element.

XX Single-strand binding protein; PUR protein; cellular oncogene;
XX eukaryotic origin of replication; gene amplification; cancer cell;
KW retinoblastoma protein; helix-destabilising protein; inhibitor;
KW hyperproliferation; c-myc; ss.

XX OS Synthetic.

XX PN WO9405689-A1.

XX PD 17-MAR-1994.

XX PF 27-AUG-1993; 93WO-US008102.

XX PR 28-AUG-1992; 92US-00938189.

XX PR 02-FEB-1993; 93US-00014943.

XX PA (MOUN) MOUNT SINAI SCHOOL MEDICINE.

XX PI Johnson EM, Bergemann AD;

XX PI WPI; 1994-101114/12.

XX Cloning and expression of PUR protein, involved in regulation of DNA
PT replication - also oligo:nucleotide(s) and antibodies for use in the
PT treatment of proliferative diseases, e.g. cancer.

XX PS Example 1; Page 37; 97pp; English.

XX Oligonucleotides AAQ44802-Q44809 were used in the characterisation of a
CC sequence element found 1.6kb upstream of the cellular c-myc gene. The PUR
CC element (see AAQ44801) is located in a region of DNA bending activity
CC which is a structural feature often associated with origins of DNA
CC replication. The PUR protein AAR50310 binds to the PUR element. (Updated
CC on 25-MAR-2003 to correct PN field.)

XX SQ Sequence 24 BP; 2 A; 14 C; 0 G; 8 T; 0 U; 0 Other;

Query Match 65.0%; Score 15.6; DB 2; Length 24;
Best Local Similarity 50.0%; Pred. No. 4.5e+03;
Matches 11; Conservative 7; Mismatches 4; Indels 0; Gaps 0;

QY 3 UUGUCUCUUCGCCACCUC 24
Db 2 TTTTCTCTCTCCCTCCACCCTC 23

RESULT 4
AAT99274
ID AAT99274 standard; DNA; 24 BP.

XX AC AAT99274;

XX DT 15-APR-1998 (first entry)

XX DE Human PUR-alpha gene probe MR0700.
 XX PI
 KW PUR element; human; c-myc; inhibitor; hyperproliferative disease; ss;
 KW cancer; probe; hybridisation.
 XX OS
 OS Synthetic.
 OS Homo sapiens.
 XX PN US5672479-A.
 XX PD 30-SEP-1997.
 XX PF 07-JUN-1995; 95US-00486421.
 XX PR 28-AUG-1992; 92US-00938189.
 PR 02-FEB-1993; 93US-00014943.
 PR 06-JUN-1995; 95US-00470911.
 XX PA (MOUN) MOUNT SINAI SCHOOL MEDICINE.
 XX PI Bergemann AD, Johnson EM;
 XX WPI; 1997-488859/45.
 XX DR Assays for PUR protein ligands or modulators - using immobilised PUR
 XX PT protein or fragments, to treat hyper-proliferative diseases, e.g. cancer.
 XX PS Example; Col 26; 64pp; English.
 XX CC The probes AAT99270-799277 were used to screen for positive clones
 CC containing a 467 bp Sau3AI fragment of the human c-myc upstream region
 CC cloned into pUC19. Isolated sequences were then used as probes to screen
 CC an expression library for sequences encoding the PUR protein. The PUR
 CC sequence can be used to identify chemical or biological compounds that
 CC bind to PUR or binding fragments of PUR. Inhibitors of PUR activity may
 CC be used to treat hyperproliferative diseases such as cancer
 XX SQ Sequence 24 BP; 2 A; 14 C; 0 G; 8 T; 0 U; 0 Other;
 Query Match 65.0%; Score 15.6; DB 2; Length 24;
 Best Local Similarity 50.0%; Pred. No. 4.5e+03;
 Matches 11; Conservative 7; Mismatches 4; Indels 0; Gaps 0;
 OY 3 UUGUCUCUCUUCGCCACCUC 24
 Db :: :|:|:| :|:|:|:|
 2 TTTTCTCTCCCTCCACCACCTC 23
 RESULT 5
 AAV31726/c
 ID AAV31726 standard; DNA; 24 BP.
 AC AAV31726;
 XX 24-SEP-1998 (first entry)
 DE Nucleotide sequence of the PUR element.
 XX PUR-alpha gene; inhibition; viral infection; cancer; PUR element;
 KW hyperproliferative disease; ss.
 XX OS Homo sapiens.
 XX PN US5756684-A.
 XX PD 26-MAY-1998.
 XX PF 06-JUN-1995; 95US-00470911.
 XX PR 28-AUG-1992; 92US-00938189.
 PR 02-FEB-1993; 93US-00014943.
 XX PA (MOUN) MOUNT SINAI SCHOOL MEDICINE.
 XX PI Bergemann AD, Johnson EM;
 XX WPI; 1998-321632/28.
 XX DR PUR protein and its fragments - that inhibit PUR protein binding to PUR
 XX PT element or other proteins.
 XX PS Example 6.1.1; Col 27; 63pp; English.
 XX CC This is the nucleotide sequence of an oligonucleotide used in the method
 CC of the invention, involving the use of the PUR protein and its fragments,
 CC which inhibit PUR protein binding to PUR element or other proteins.
 CC Inhibitors of PUR activity may be useful for treating viral infections
 CC and hyperproliferative diseases such as cancer
 XX SQ Sequence 24 BP; 2 A; 14 C; 0 G; 8 T; 0 U; 0 Other;
 Query Match 65.0%; Score 15.6; DB 2; Length 24;
 Best Local Similarity 50.0%; Pred. No. 4.5e+03;
 Matches 11; Conservative 7; Mismatches 4; Indels 0; Gaps 0;
 OY 3 UUGUCUCUCUUCGCCACCUC 24
 Db :: :|:|:| :|:|:|:|
 2 TTTTCTCTCCCTCCACCACCTC 23

PA (MOUN) MOUNT SINAI SCHOOL MEDICINE.
 XX Bergemann AD, Johnson EM;
 XX WPI; 1998-321632/28.
 XX PT PUR protein and its fragments - that inhibit PUR protein binding to PUR
 XX PT element or other proteins.
 XX PS Disclosure; Col 12; 63pp; English.
 XX CC This is the nucleotide sequence of the PUR element used in the method of
 CC the invention, involving the use of the PUR protein and its fragments,
 CC which inhibit PUR protein binding to PUR element or other proteins.
 CC Inhibitors of PUR activity may be useful for treating viral infections
 CC and hyperproliferative diseases such as cancer
 XX SQ Sequence 24 BP; 8 A; 0 C; 14 G; 2 T; 0 U; 0 Other;
 Query Match 65.0%; Score 15.6; DB 2; Length 24;
 Best Local Similarity 50.0%; Pred. No. 4.5e+03;
 Matches 11; Conservative 7; Mismatches 4; Indels 0; Gaps 0;
 OY 3 UUGUCUCUCUUCGCCACCUC 24
 Db :: :|:|:| :|:|:|:|
 23 TTTTCTCTCCCTCCACCACCTC 23
 RESULT 6
 AAV31731
 ID AAV31731 standard; DNA; 24 BP.
 AC AAV31731;
 XX 24-SEP-1998 (first entry)
 DE Nucleotide sequence of the oligonucleotide MR0700.
 XX PUR-alpha gene; inhibition; viral infection; cancer; PUR element;
 KW hyperproliferative disease; ss.
 XX OS Synthetic.
 XX PN US5756684-A.
 XX PD 26-MAY-1998.
 XX PF 06-JUN-1995; 95US-00470911.
 XX PR 28-AUG-1992; 92US-00938189.
 PR 02-FEB-1993; 93US-00014943.
 XX PA (MOUN) MOUNT SINAI SCHOOL MEDICINE.
 XX PI Bergemann AD, Johnson EM;
 XX WPI; 1998-321632/28.
 XX DR PUR protein and its fragments - that inhibit PUR protein binding to PUR
 XX PT element or other proteins.
 XX PS Example 6.1.1; Col 27; 63pp; English.
 XX CC This is the nucleotide sequence of an oligonucleotide used in the method
 CC of the invention, involving the use of the PUR protein and its fragments,
 CC which inhibit PUR protein binding to PUR element or other proteins.
 CC Inhibitors of PUR activity may be useful for treating viral infections
 CC and hyperproliferative diseases such as cancer
 XX SQ Sequence 24 BP; 2 A; 14 C; 0 G; 8 T; 0 U; 0 Other;
 Query Match 65.0%; Score 15.6; DB 2; Length 24;
 Best Local Similarity 50.0%; Pred. No. 4.5e+03;
 Matches 11; Conservative 7; Mismatches 4; Indels 0; Gaps 0;

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Matches 11; Conservative 7; Mismatches 4; Indels 0; Gaps 0;

Qy 3 UUGUCUCUCCUUGGCCACCUC 24
Db 2 TTTTCTCTCCCTCCACCACCTC 23

RESULT 7
AAX04070/c
ID AAX04070 standard; DNA; 24 BP.
XX AC
XX AC AAX04070;
DT 12-APR-1999 (first entry)
XX DE
XX DE Oligonucleotide MF0677 used in PUR identification/characterisation.
XX KW
XX KW PUR element; PUR-alpha; hyperproliferative disease; cancer; human;
XX KW monoclonal antibody; identification; characterisation; ss.
XX OS
XX OS Synthetic.
XX OS Homo sapiens.
XX PN
XX PN US5869622-A.
XX PD
XX PD 09-FEB-1999.
XX PF
XX PF 07-JUN-1995; 95US-00486809.
XX PR
XX PR 28-AUG-1992; 92US-00938189.
XX PR 02-FEB-1993; 93US-00014943.
XX PR 06-JUN-1995; 95US-00470911.
XX PA (MOUN ) MOUNT SINAI SCHOOL MEDICINE.
XX PI Bergemann AD, Johnson EM;
XX PI WPI; 1999-152881/13.
XX PN
XX PN Monoclonal antibody specific for PUR protein - useful for treating
XX PT cancer.
XX PS
XX PS Example; Col 27; 64pp; English.
XX CC
XX CC The present invention describes a monoclonal antibody that specifically
XX CC binds to an epitope of the PUR protein. Antibodies that bind to the PUR
XX CC protein and neutralise PUR activity may be used to treat
XX CC hyperproliferative diseases such as cancer. PUR antibodies may be used
XX CC diagnostically to detect aberrant expression of the PUR protein and/or
XX CC mutations in the PUR gene. The present sequence represents an
XX CC oligonucleotide used in the identification and characterisation of the
XX CC PUR protein and its sequence element PUR repeat, in an example from the
XX CC present invention
XX SQ Sequence 24 BP; 8 A; 0 C; 14 G; 2 T; 0 U; 0 Other;

Query Match 65.0%; Score 15.6; DB 2; Length 24;
Best Local Similarity 50.0%; Pred. No. 4.5e+03;
Matches 11; Conservative 7; Mismatches 4; Indels 0; Gaps 0;

Qy 3 UUGUCUCUCCUUGGCCACCUC 24
Db 2 TTTTCTCTCCCTCCACCACCTC 23

RESULT 8
AAX04075
ID AAX04075 standard; DNA; 24 BP.
XX AC
XX AC AAX04075;
DT 12-APR-1999 (first entry)
XX DE
XX DE 12-APR-1999 (first entry)
XX KW
XX KW chromatin; DNA hybridization; DNA amplification; DNA microarray;
XX KW diagnosis; ss; primer; PCR; OLIG2.
XX OS
XX OS Homo sapiens.
XX PN
XX PN WO2005118873-A2.
XX PD
XX PD 15-DEC-2005.
XX PF
XX PF 31-MAY-2005; 2005WO-US019150.
XX PR
XX PR 28-MAY-2004; 2004US-0575478P.
XX
```

```
DE Oligonucleotide MR0700 used in PUR identification/characterisation.
XX PUR element; PUR-alpha; hyperproliferative disease; cancer; human;
XX KW monoclonal antibody; identification; characterisation; ss.
XX OS
XX OS Synthetic.
XX OS Homo sapiens.
XX PN
XX PN US5869622-A.
XX PD
XX PD 09-FEB-1999.
XX PF
XX PF 07-JUN-1995; 95US-00486809.
XX PR
XX PR 28-AUG-1992; 92US-00938189.
XX PR 02-FEB-1993; 93US-00014943.
XX PR 06-JUN-1995; 95US-00470911.
XX PA (MOUN ) MOUNT SINAI SCHOOL MEDICINE.
XX PI Bergemann AD, Johnson EM;
XX PI WPI; 1999-152881/13.
XX PN
XX PN Monoclonal antibody specific for PUR protein - useful for treating
XX PT cancer.
XX PS
XX PS Example; Col 27; 64pp; English.
XX CC
XX CC The present invention describes a monoclonal antibody that specifically
XX CC binds to an epitope of the PUR protein. Antibodies that bind to the PUR
XX CC protein and neutralise PUR activity may be used to treat
XX CC hyperproliferative diseases such as cancer. PUR antibodies may be used
XX CC diagnostically to detect aberrant expression of the PUR protein and/or
XX CC mutations in the PUR gene. The present sequence represents an
XX CC oligonucleotide used in the identification and characterisation of the
XX CC PUR protein and its sequence element PUR repeat, in an example from the
XX CC present invention
XX SQ Sequence 24 BP; 2 A; 14 C; 0 G; 8 T; 0 U; 0 Other;

Query Match 65.0%; Score 15.6; DB 2; Length 24;
Best Local Similarity 50.0%; Pred. No. 4.5e+03;
Matches 11; Conservative 7; Mismatches 4; Indels 0; Gaps 0;

Qy 3 UUGUCUCUCCUUGGCCACCUC 24
Db 2 TTTTCTCTCCCTCCACCACCTC 23

RESULT 9
AEE94315/c
ID AEE94315 standard; DNA; 25 BP.
XX AC
XX AC AEE94315;
XX DT
XX DT 23-FEB-2006 (first entry)
XX DE
XX DE 3' primer for PCR of DNase I treated OLIG2 chromatin.
XX KW
XX KW chromatin; DNA hybridization; DNA amplification; DNA microarray;
XX KW diagnosis; ss; primer; PCR; OLIG2.
XX OS
XX OS Homo sapiens.
XX PN
XX PN WO2005118873-A2.
XX PD
XX PD 15-DEC-2005.
XX PF
XX PF 31-MAY-2005; 2005WO-US019150.
XX PR
XX PR 28-MAY-2004; 2004US-0575478P.
XX
```


CC polarisation or charge. The enzyme is useful for cleaving a nucleic acid
CC which involves exposing a sample (a cell lysate) comprising substrate
CC nucleic acid to the enzyme which produces at least one detectable
CC cleavage product. The enzyme is employed for detecting target DNAs and
CC RNAs comprising wild-type and mutant alleles of genes including genes
CC from humans, other animal or plants that are or may be associated with
CC disease or other conditions. In addition, the enzymes may be useful for
CC detecting and identifying strains of microorganisms including bacteria,
CC fungi, protozoa, ciliates and viruses, preferably detecting and
CC identifying viruses having RNA genomes, such as hepatitis C and human
CC immunodeficiency virus.

XX
XX
SQ Sequence 28 BP; 3 A; 11 C; 4 G; 10 T; 0 U; 0 Other;

Query Match 63.3%; Score 15.2; DB 7; Length 28;
Best Local Similarity 50.0%; Pred. No. 6.8e+03;
Matches 10; Conservative 7; Mismatches 3; Indels 0; Gaps 0;

Qy 5 GUCUCUCUUCGCGCCACUC 24
|:|:|:|:|:|:|:|:|:|
Db 8 GTCTCTCTTTGCCAGTTC 27

RESULT 14
AAV91451/c
ID AAV91451 standard; RNA; 29 BP.
XX
XX
AC AAV91451;
XX
XX
DT 18-FEB-1999 (first entry)
XX
XX
DE Human C-raf hammerhead ribozyme nucleotide position 220.
XX
XX
KW Human; c-raf; A-raf; B-raf; hammerhead ribozyme; hairpin ribozyme;
KW target; substrate; catalyst; modulation; expression; Raf gene; delivery;
KW screening; identification; synthesis; deprotection; purification; cancer;
KW inflammation; psoriasis; non-hepatic acites; infection; genetic drift;
KW reutenosis; rheumatoid arthritis; ss.
XX
XX
OS Synthetic.
OS Homo sapiens.
OS
PN WO9850530-A2.
XX
XX
PD 12-NOV-1998.
XX
XX
PF 05-MAY-1998; 98WO-US009249.
XX
XX
PR 09-MAY-1997; 97US-0046059P.
PR 09-JUN-1997; 97US-0049002P.
PR 03-JUL-1997; 97US-0051718P.
PR 22-AUG-1997; 97US-0056808P.
PR 02-OCT-1997; 97US-0061321P.
PR 02-OCT-1997; 97US-0061324P.
PR 05-NOV-1997; 97US-0064866P.
PR 19-DEC-1997; 97US-0068212P.
XX
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
XX
PI Jarvis T, Matulic-Adamic J, Reynolds M, Kisich K, Bellon L;
PI Parry T, Beigelman L, Mcswiggen JA, Karpeisky A, Burgin A;
PI Thompson J, Workman CT, Beaudy A, Sweedler D;
XX
XX
DR WPI; 1999-009494/01.
XX
XX
PT Identifying new catalytic nucleic acid that modulates selected processes
PT - especially ribozymes that cleave Raf RNA for treating cancer,
PT reutenosis, and also new ribozymes and modified nucleoside triphosphates
PT used as antiviral agents and synthons.
XX
XX
XX Claim 151; Page 146; 259pp; English.
XX
XX
CC A method has been developed for the identification of a nucleic acid

CC capable of modulating a process in a biological system. The method
CC comprises: (a) introducing into the system a random library of nucleic
CC acid catalysts (NAC) having a substrate binding domain (SBD), comprising
CC a random sequence, and a catalytic domain (CD); and (b) identifying NAC
CC in systems where modulation has occurred and/or determining the sequence
CC of at least part of the SBDs in such systems. Nucleic acid molecules with
CC endonuclease activity and catalytic activity, from the present invention,
CC are used to modulate gene expression in plant and mammalian cells and to
CC cleave target nucleic acid, particularly for treating systemic diseases
CC caused by specific RNA, e.g. cancer, inflammation, psoriasis, non-hepatic
CC ascites and infection. They may also be used to detect genetic drift and
CC mutations in diseased cells and to determine c-raf RNA. Specifically NACs
CC with RNA-cleaving activity that modulate expression of the Raf gene, are
CC used to treat cancer, restenosis, psoriasis or rheumatoid arthritis, or
CC generally any condition associated with the level of c-raf. Introduction
CC of sugar/phosphate modifications increases stability against nuclease and
CC activity. AAV90922 to AAV93877 represent NACs that can be used in the
CC method, specifically for modulating the expression of a Raf gene
XX
XX Sequence 29 BP; 11 A; 3 C; 9 G; 0 T; 5 U; 1 Other;

Query Match 61.7%; Score 14.8; DB 2; Length 29;
Best Local Similarity 47.4%; Pred. No. 1e+04;
Matches 9; Conservative 7; Mismatches 3; Indels 0; Gaps 0;

QY 6 UCUCUCUUUCGCCACCUC 24
Db 29 TCTCTCCTTTTCGNCTCATC 11

RESULT 15
AAF01081/c

ID AAF01081 standard; RNA; 29 BP.

XX AC
XX AAF01081;

DT 16-FEB-2001 (first entry)

XX Hammerhead ribozyme #1072.

DE Ribozyme; erythropoietin; granulocyte colony stimulating factor;

KW interferon alpha; ss.

XX Homo sapiens.

XX WO200061729-A2.

XX 19-OCT-2000.

XX 11-APR-2000; 2000WO-US009721.

XX 12-APR-1999; 99US-0129390P.

XX (RIBO-) RIBOZYME PHARM INC.

XX Blatt L, Zwick M, Pavco P, Meswiggen J;

XX WPI; 2000-647423/62.

XX Enzymatic and antisense nucleic acid inhibition of repressor genes,
PT useful for producing e.g. granulocyte colony stimulating factor protein,
PT interferon alpha and erythropoietin.

XX Claim 32; Page 80; 164pp; English.

XX The present invention relates to enzymatic and antisense nucleic acid
XX molecules that act as inhibitors of the expression of repressor genes
CC encoding the TR2 Orphan receptor, EAR3/COUP-1F-1, the GATA transcription
CC factor gene, IRF-2 and/or the C/EBP Displacement Protein (CDP).
CC Inhibition of the repressors removes prevents inhibition (and
CC consequently increases expression of) genes involved in the production of
CC erythropoietin, granulocyte colony stimulating factor protein and
CC interferon alpha

XX
SQ Sequence 29 BP; 13 A; 2 C; 9 G; 0 T; 4 U; 1 Other;
Query Match 61.7%; Score 14.8; DB 3; Length 29;
Best Local Similarity 47.4%; Pred. No. 1e+04;
Matches 9; Conservative 7; Mismatches 3; Indels 0; Gaps 0;

QY 6 UCUCUCUUUCGCCACCUC 24
Db 29 TCTCTCCTTTTCGNCTCATC 11

Search completed: October 16, 2006, 14:16:00
Job time : 126.594 secs

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C 2	15.6	65.0	24	2	AR010025	AR010025 Sequence
C 3	15.6	65.0	24	2	AR034743	AR034743 Sequence
C 4	15.6	65.0	24	2	AR034760	AR034760 Sequence
C 5	15.6	65.0	24	2	124740	124740 Sequence 3
C 6	15.6	65.0	24	2	124752	124752 Sequence 1
C 7	14.8	61.7	29	2	BD253279	BD253279 Regulatory
C 8	14.8	61.7	29	2	AR265215	AR265215 Sequence
C 9	14.4	60.0	18	2	AR072296	AR072296 Sequence
C 10	14.4	60.0	18	2	126407	126407 Sequence 9
C 11	14.2	59.2	21	2	128585	128585 Sequence 3
C 12	14.2	59.2	21	2	158747	158747 Sequence 3
C 13	14.2	59.2	25	2	AX649750	AX649750 Sequence
C 14	14.2	59.2	25	2	AX649751	AX649751 Sequence
C 15	14.2	59.2	25	2	AX649752	AX649752 Sequence
C 16	14.2	59.2	25	2	AX649753	AX649753 Sequence
C 17	14.2	59.2	25	2	AX649754	AX649754 Sequence
C 18	14.2	59.2	25	2	AX649755	AX649755 Sequence


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ORIGIN
Query Match          59.2%; Score 14.2; DB 2; Length 21;
Best Local Similarity 36.8%; Pred. No. 8.1e+04;
Matches 7; Conservative 9; Mismatches 3; Indels 0; Gaps 0;
QY 1 UAUUGUCUCUCUUGGCC 19
Db 19 TTTATCTCTCCTTTCTCC 1

RESULT 12
I58747/c
LOCUS          21 bp      DNA      linear      PAT 07-OCT-1997
DEFINITION     Sequence 38 from patent US 5652350.
ACCESSION      I58747
VERSION        I58747.1 GI:2477985
KEYWORDS       .
SOURCE         Unknown.
ORGANISM       Unknown.
REFERENCE      1 (bases 1 to 21)
AUTHORS       Watanabe,K.A., Ren,W.-Y. and Weil,R.
TITLE         Complementary DNA and toxins
JOURNAL       Patent: US 5652350-A 38 29-JUL-1997;
FEATURES       Location/Qualifiers
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ORIGIN
Query Match          59.2%; Score 14.2; DB 2; Length 21;
Best Local Similarity 36.8%; Pred. No. 8.1e+04;
Matches 7; Conservative 9; Mismatches 3; Indels 0; Gaps 0;
QY 1 UAUUGUCUCUCUUGGCC 19
Db 19 TTTATCTCTCCTTTCTCC 1

RESULT 13
AX649750/c
LOCUS          25 bp      DNA      linear      PAT 22-MAR-2003
DEFINITION     Sequence 1590 from Patent EP1273660.
ACCESSION      AX649750
VERSION        AX649750.1 GI:29152568
KEYWORDS       .
SOURCE         Homo sapiens (human)
ORGANISM       Homo sapiens
                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                Hominidae; Homo.
REFERENCE      1
AUTHORS       Gu,Y.
TITLE         Human sodium-hydrogen exchanger like protein 1
JOURNAL       Patent: EP 1273660-A 1590 08-JAN-2003;
FEATURES       Location/Qualifiers
                source
                1..25
                /organism="Homo sapiens"
                /mol_type="unassigned DNA"
                /db_xref="taxon:9606"

ORIGIN
Query Match          59.2%; Score 14.2; DB 2; Length 25;
Best Local Similarity 52.6%; Pred. No. 8.2e+04;
Matches 10; Conservative 6; Mismatches 3; Indels 0; Gaps 0;
QY 2 AUUGUCUCUCUUGGCCA 20
Db 25 ACTGTCCTCCATTCCTCC 7

RESULT 14
AX649751/c
LOCUS          25 bp      DNA      linear      PAT 22-MAR-2003
DEFINITION     Sequence 1591 from Patent EP1273660.
ACCESSION      AX649751
VERSION        AX649751.1 GI:29152569
KEYWORDS       .
SOURCE         Homo sapiens (human)
ORGANISM       Homo sapiens
                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                Hominidae; Homo.
REFERENCE      1
AUTHORS       Gu,Y.
TITLE         Human sodium-hydrogen exchanger like protein 1
JOURNAL       Patent: EP 1273660-A 1591 08-JAN-2003;
FEATURES       Location/Qualifiers
                source
                1..25
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                /mol_type="unassigned DNA"
                /db_xref="taxon:9606"

ORIGIN
Query Match          59.2%; Score 14.2; DB 2; Length 25;
Best Local Similarity 52.6%; Pred. No. 8.2e+04;
Matches 10; Conservative 6; Mismatches 3; Indels 0; Gaps 0;
QY 2 AUUGUCUCUCUUGGCCA 20
Db 23 ACTGTCCTCCATTCCTCC 5

Search completed: October 16, 2006, 14:52:15
Job time : 591.797 secs
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GenCore version 5.1.9
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OM nucleic - nucleic search, using sw model

Run on: October 16, 2006, 14:04:23 ; Search time 1032.18 Seconds
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Title: US-10-604-726A-5136
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Total number of hits satisfying chosen parameters: 56556

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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C 3	13	54.2	28	1	A1673609	A1673609 we76d05.x	
C 4	12.8	53.3	29	13	CL983097	CL983097 GC0336 TI	
C 5	12.4	51.7	30	11	A2604126	A2604126 IM0423013	
C 6	12.2	50.8	24	4	CA850924	CA850924 D08B11 D2	
C 7	12.2	50.8	27	11	A2340258	A2340258 IM0072C20	
C 8	12	50.0	23	11	A2329650	A2329650 IM0054A13	
C 9	12	50.0	23	11	A2514958	A2514958 IM0054A13	
C 10	12	50.0	27	13	CL983109	CL983109 GC0348 TI	
C 11	12	50.0	28	11	BH901484	BH901484 SALK 0796	
C 12	11.8	49.2	28	14	DMF545811	AJ545811 Drosophila	
C 13	11.6	48.3	25	11	A1539240	AZ475883 IM0294J14	
C 14	11.6	48.3	25	1	A1539240	A1539240 tp64b08.x	
C 15	11.6	48.3	26	11	AZ454352	AZ454352 IM0256G18	
C 16	11.6	48.3	28	1	A1183010	A1183010 ub92e02.r	
C 17	11.6	48.3	29	11	AZ780850	AZ780850 2M0018A02	
C 18	11.6	48.3	29	11	AZ828692	AZ828692 2M0105N15	
C 19	11.4	47.5	27	11	AZ432080	AZ432080 IM0217024	

20	11.4	47.5	28	1	A1118404	A1118404 ue36c02.x	
21	11.4	47.5	28	11	AZ342196	AZ342196 IM0075F07	
C 22	11.4	47.5	28	14	TA205E06P	AL479131 T. brucei	
23	11.4	47.5	29	11	AZ345594	AZ345594 IM0080016	
24	11.4	47.5	29	13	CZ472219	CZ472219 d01414-5p	
C 25	11.4	47.5	30	13	CZ477542	CZ477542 d11088-5p	
C 26	11.2	46.7	18	8	CN750241	CN750241 ApDT-VIII	
C 27	11.2	46.7	21	14	AG189071	AG189071 Pan trogl	
28	11.2	46.7	21	14	AG202804	AG202804 Pan trogl	
C 29	11.2	46.7	22	8	CO788412	CO788412 NT004A GO	
C 30	11.2	46.7	25	13	CL692271	CL692271 PRI0158C	
C 31	11.2	46.7	27	11	AZ416143	AZ416143 IM0191G14	
C 32	11.2	46.7	27	14	AG198505	AG198505 Pan trogl	
C 33	11.2	46.7	28	11	AZ829200	AZ829200 2M0106N11	
C 34	11.2	46.7	29	12	BZ593222	BZ593222 SALK 0682	
C 35	11.2	46.7	30	13	CZ175615	CZ175615 MIAA-6F19	
C 36	11	45.8	19	13	CL671134	CL671134 PRI0163d	
C 37	11	45.8	22	1	AU014100	AU014100 AU014100 -	
38	11	45.8	22	1	AU014106	AU014106 AU014106	
39	11	45.8	22	11	AZ942905	AZ942905 2M0203K13	
C 40	11	45.8	23	14	CT014183	CT014183 KBRH122F2	
41	11	45.8	27	14	TA204D03P	AL476477 T. brucei	
42	11	45.8	30	11	AZ976285	AZ976285 2M0251H09	
C 43	10.8	45.0	25	1	A1527253	A1527253 u350e07.x	
44	10.8	45.0	25	11	AZ479489	AZ479489 IM0300H08	
45	10.8	45.0	27	11	AZ949222	AZ949222 2M0212A12	

ALIGNMENTS

RESULT 1
AZ775852/c
LOCUS
DEFINITION 25 bp DNA linear GSS 16-FEB-2001
clone UUGC2M0009N01 F, genomic survey sequence.

ACCESSION AZ775852
VERSION AZ775852.1 GI:12902821

KEYWORDS
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

REFERENCE
AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0009 row: N column: 01
Seq primer: CGTTGTAAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 25.

FEATURES
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1..25
Location/Qualifiers
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0009N01"
/sex="Male"

/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_lib="mouse 10kb plasmid UUGCIM library"
 /note="Vector: PWD42nv, Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 55.8%; Score 13.4; DB 11; Length 25;
 Best Local Similarity 43.5%; Pred. No. 3.3e+05;
 Matches 10; Conservative 7; Mismatches 6; Indels 0; Gaps 0;

QY 2 AUGUGUCUCCUUUGCCACCUC 24

Db :::::|||||

24 ATTCATCTCCTTTCACACCCC 2

RESULT 2

BQ586604/c

LOCUS

DEFINITION E012388-024-012-E21-SP6 MP12-ADIS-024-leaf Beta vulgaris cDNA clone 024-012-E21 5-PRIME, mRNA sequence.

ACCESSION BQ586604

VERSION BQ586604.1

KEYWORDS GI:26116186

SOURCE Beta vulgaris

ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; Caryophyllales; Amaranthaceae; Beta.

REFERENCE 1 (bases 1 to 26)

Herwig, R., Schulz, B., Weisshaar, B., Hennig, S., Steinfath, M., Drungowski, M., Stahl, D., Wruck, W., Menze, A., O'Brien, J., Lehrach, H. and Radelof, U.

TITLE Construction of a 'unigene' cDNA clone set by oligonucleotide fingerprinting allows access to 25 000 potential sugar beet genes

JOURNAL Plant J. 32 (5), 845-857 (2002)

PUBMED 12472698

COMMENT Contact: Weisshaar B

ADIS DNA core facility at MPIZ

Max-planck-Institute for Plant Breeding Research

Carl-von-Linne Weg 10, 50829 Koeln, Germany

Fax: 00492215062851

Email: weisshaar@mpiz-koeln.mpg.de

Insert Length: 26 Std Error: 0.00

Plate: 12 row: E column: 21

Seq primer: SP6; CATACGATTAGTGACACTATAG.

Location/Qualifiers

1..26

/organism="Beta vulgaris"

/mol_type="mRNA"

/cultivar="KWS2320 (double haploid, monogerm breeding line)"

/db_xref="GABI:186264"

/db_xref="taxon:161934"

/clone="024-012-E21"

/tissue_type="leaf"

/lab_host="EMDH10B"

/clone_lib="MPIZ-ADIS-024-leaf"
 /note="Vector: pCMVSPORT6; Site 1: SalI; Site 2: NotI;
 cDNA library from sugar beet. Library provided by KWS
 Kleinwanzlebener Saatucht AG Einbeck, Germany, contact:
 b.schulz@kws.de; cloning sites SalI-NotI, primer sites and
 orientation:
 SP6-SalI-CCACGCGTCG-5prime-cDNA-polyA-CC-NotI-T7; Note:
 Sequencing granted in the context of the GABI-Beet
 project, local PI: Dr. Katharina Schneider, coordinator:
 Prof. Christian Jung; Sequence submission managed by
 RZPD/GABI-Primary database:http://gabi.rzpd.de"

ORIGIN

Query Match 55.8%; Score 13.4; DB 3; Length 26;
 Best Local Similarity 47.8%; Pred. No. 3.3e+05;
 Matches 11; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

QY 2 AUGUGUCUCCUUUGCCACCUC 24

Db :::::|||||

23 ATATTCTGCGCTTCTCCCCCC 1

RESULT 3

AI673609

LOCUS

DEFINITION AI673609 28 bp mRNA linear EST 19-DEC-1999
 we76d05.xl Soares Dieckgraebe colon NHCD Homo sapiens cDNA clone
 IMAGE:2347017 3' similar to TR:060318 O60318 MCM3 IMPORT FACTOR ;,
 mRNA sequence.

ACCESSION AI673609

VERSION AI673609.1

KEYWORDS GI:4853340

SOURCE EST.

ORGANISM Homo sapiens (human)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

Hominidae; Homo.

REFERENCE 1 (bases 1 to 28)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

AUTHORS National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

Tumor Gene Index

Unpublished (1997)

Contact: Robert Strausberg, Ph.D.

Email: cgsb@rs-mail.nih.gov

This clone is available royalty-free through LLNL; contact the

IMAGE Consortium (info@image.llnl.gov) for further information.

Trace considered overall poor quality

Insert Length: 850 Std Error: 0.00

Seq primer: -40UP from Gibco

High quality sequence stop: 1.

Location/Qualifiers

1..28

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:2347017"

/tissue_type="colonic mucosa from 3 patients with Crohn's

disease"

/lab_host="DH10B (phage-resistant)"

/clone_lib="Soares_Dieckgraebe_colon NHCD"

/note="Organ: colon; Vector: pT73b-Paci; Site 1: Not I;

Site 2: Eco RI; 1st strand cDNA was primed with a Not I -

oligo(dT) primer [5'

TGTTACCAATCTGAAGTGGAGCGCGCCGCTTTTTTTTTTTT 3'],

double-stranded cDNA was ligated to Eco RI adaptors

(Pharmacia), digested with Not I and cloned into the Not I

and Eco RI sites of the modified pT73 vector. Library

went through one round of normalization. Tissue samples

provided by Dr. Brian Dieckgraebe (Washington University,

dieck@im.wustl.edu); colonic mucosa represents a range of

disease involvement from moderate to severe Crohn's

disease; samples include both perforating (fistulas) and

non-perforating samples. Library constructed by Bento

Soares and M. Fatima Bonaldo."

FEATURES

source

ORIGIN	Query Match	54.2%;	Score 13;	DB 1;	Length 28;
	Best Local Similarity	38.1%;	Pred. No. 5e+05;		
	Matches	8;	Conservative	8;	Mismatches 5; Indels 0; Gaps 0;
Qy	1	UAUUGUCUCCUUGCCACC 21			
	8	TCTGTCTCTCTCTTCTCCAC 28			
Db					
RESULT 4	CL983097/c				
	LOCUS	29 bp	mRNA	linear	GSS 21-SEP-2004
	DEFINITION	GC0336 TIGEM gene trap library Mus musculus cDNA clone 10662.60,			
ACCESSION	CL983097				
	VERSION	CL983097.1	GI:52420677		
KEYWORDS	SOURCE	Mus musculus (house mouse)			
	ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridea; Muridae; Murinae; Mus.			
REFERENCE	AUTHORS	Cobellis, G., Nicolaus, G., Iovino, M., Romito, A., Marra, E., Barbarisi, M., Sardiello, M., Di Giorgio, F.P., Iovino, N., Zollo, M., Ballabio, A. and Cortese, R.			
	TITLE	Tagging genes with cassette-exchange sites			
JOURNAL	PUBLISHED	Nucleic Acids Res. 33 (4), e44 (2005)			
	COMMENT	15741177			
FEATURES	source	1..29			
	Location/Qualifiers	Via P. Castellino, 111, 80131 NAPOLI, ITALY			
ORIGIN	Query Match	53.3%;	Score 12.8;	DB 13;	Length 29;
	Best Local Similarity	58.8%;	Pred. No. 6.2e+05;		
Qy	8	UCUCCUUUGCCACCUC 24			
	21	TCGCCATTGCCCANCTC 5			
Db					
RESULT 5	AZ604126/c				
	LOCUS	30 bp	DNA	linear	GSS 13-DEC-2000
	DEFINITION	IM0423013R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0423013 R, genomic survey sequence.			
ACCESSION	AZ604126				
	VERSION	AZ604126.1	GI:11726316		

KEYWORDS	GSS.				
	Mus musculus (house mouse)				
	ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridea; Muridae; Murinae; Mus.			
REFERENCE	AUTHORS	Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.			
	TITLE	Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts			
JOURNAL	COMMENT	Unpublished (2000)			
	Contact: Robert B. Weiss				
FEATURES	source	1..30			
	Location/Qualifiers	Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA			
ORIGIN	Query Match	51.7%;	Score 12.4;	DB 11;	Length 30;
	Best Local Similarity	40.9%;	Pred. No. 9.3e+05;		
Qy	3	UUGUCUCCUCCUUGCCACCUC 24			
	28	TTGCCTCACCCTTCCTCTCTC 7			
Db					
RESULT 6	CA850924				
	LOCUS	24 bp	mRNA	linear	EST 01-AUG-2003
	DEFINITION	D08B11.D23 04.ab1 cDNA Peking library 2, 4 day SCN3 Glycine max cDNA clone D08B11 5', mRNA sequence.			
ACCESSION	CA850924				
	VERSION	CA850924			

```

VERSION
KEYWORDS
SOURCE
ORGANISM

FEATURES
    source
        1. 24
            /organism="Glycine max"
            /mol_type="mRNA"
            /cultivar="Peking"
            /db_xref="taxon:3847"
            /clone="D08B11"
            /tissue_type="Roots"
            /dev_stage="Seedlings"
            /clone_lib="cDNA Peking library 2, 4 day SCN3"
            /notes="Vector: pBluescript SK-; cDNA clones from mRNA
            extracted from Peking roots 2 and 4 days past invasion."

ORIGIN
    Query Match          50.8%; Score 12.2; DB 4; Length 24;
    Best Local Similarity 47.1%; Pred. No. 1.1e+06;
    Matches 8; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

QY 7 CUCUCUUCGCCACCU 23
    |||: |||: |||:
Db 5 CTCTCTTTCCTACCT 21

RESULT 7
AZ340258/c
LOCUS
DEFINITION
    AZ340258 1M0072C20F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
    clone UUGC1M0072C20 F, genomic survey sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
    Mus musculus (house mouse)
    Mus musculus
    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
    Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
    Sciurognathi; Murioidea; Muridae; Murinae; Mus.
REFERENCE
    1 (bases 1 to 27)
    Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
    Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
    Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
    Niederhausern,A. and Wright,D.,Weiss,R.
    Mouse whole genome scaffolding with paired end reads from 10kb
    plasmid inserts
    Unpublished (2000)
    Contact: Robert B. Weiss
    University of Utah Genome Center
    University of Utah
    Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
    84112, USA
    Tel: 801 585 5606
    Fax: 801 585 7177

AZ340258
LOCUS
DEFINITION
    AZ340258 27 bp DNA linear GSS 29-SEP-2000
    clone UUGC1M0072C20 F, genomic survey sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
    Mus musculus (house mouse)
    Mus musculus
    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
    Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
    Sciurognathi; Murioidea; Muridae; Murinae; Mus.
REFERENCE
    1 (bases 1 to 27)
    Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
    Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
    Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
    Niederhausern,A. and Wright,D.,Weiss,R.
    Mouse whole genome scaffolding with paired end reads from 10kb
    plasmid inserts
    Unpublished (2000)
    Contact: Robert B. Weiss
    University of Utah Genome Center
    University of Utah
    Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
    84112, USA
    Tel: 801 585 5606
    Fax: 801 585 7177

AZ340258
LOCUS
DEFINITION
    AZ340258 23 bp DNA linear GSS 29-SEP-2000
    clone UUGC1M0054A13 R, genomic survey sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
    Mus musculus (house mouse)
    Mus musculus
    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
    Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
    Sciurognathi; Murioidea; Muridae; Murinae; Mus.
REFERENCE
    1 (bases 1 to 23)
    Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
    Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
    Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
    Niederhausern,A. and Wright,D.,Weiss,R.
    Mouse whole genome scaffolding with paired end reads from 10kb
    plasmid inserts
    Unpublished (2000)
    Contact: Robert B. Weiss
    University of Utah Genome Center
    University of Utah
    Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
    84112, USA
    Tel: 801 585 5606
    Fax: 801 585 7177

Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0072 row: C column: 20
Seq primer: CCGTGTAAACACGCGCCAGT
Class: plasmid ends
High quality sequence stop: 27.
Location/Qualifiers
    1. 27
        /organism="Mus musculus"
        /mol_type="genomic DNA"
        /strains="C57BL/6J"
        /db_xref="taxon:10090"
        /clone="UUGC1M0072C20"
        /sex="Male"
        /lab_host="E. Coli strain XL10-Gold, TI-resistant, F-"
        /clone_lib="Mouse 10kb plasmid UUGC1M library"
        /note="Vector: PWD42nv; Purified genomic DNA from M.
        musculus C57BL/6J (male) was obtained from the Jackson
        Laboratory Mouse DNA Resource
        (http://www.jax.org/resources/documents/dnares/). The DNA
        was hydrodynamically sheared by repeated passage through a
        0.005 inch orifice at constant velocity. The sheared DNA
        was blunt end-repaired with T4 DNA polymerase and T4
        polynucleotide kinase. Adaptor oligonucleotides were
        ligated to the blunt ends in high molar excess. The
        adaptor DNA was purified and size-selected for a 9.5 to
        10.5 kb range using preparative agarose gel
        electrophoresis. Vector DNA was prepared from a derivative
        of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
        inducible derivative of plasmid R1. The vector was ligated
        with adaptors complementary to the insert adaptors and
        purified. The sheared, adaptor mouse DNA was annealed to
        adaptor vector DNA, and transformed into
        chemically-competent E. coli XL10-Gold (Stratagene) cells
        and selected for ampicillin resistance."

Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0072 row: C column: 20
Seq primer: CCGTGTAAACACGCGCCAGT
Class: plasmid ends
High quality sequence stop: 27.
Location/Qualifiers
    1. 27
        /organism="Mus musculus"
        /mol_type="genomic DNA"
        /strains="C57BL/6J"
        /db_xref="taxon:10090"
        /clone="UUGC1M0072C20"
        /sex="Male"
        /lab_host="E. Coli strain XL10-Gold, TI-resistant, F-"
        /clone_lib="Mouse 10kb plasmid UUGC1M library"
        /note="Vector: PWD42nv; Purified genomic DNA from M.
        musculus C57BL/6J (male) was obtained from the Jackson
        Laboratory Mouse DNA Resource
        (http://www.jax.org/resources/documents/dnares/). The DNA
        was hydrodynamically sheared by repeated passage through a
        0.005 inch orifice at constant velocity. The sheared DNA
        was blunt end-repaired with T4 DNA polymerase and T4
        polynucleotide kinase. Adaptor oligonucleotides were
        ligated to the blunt ends in high molar excess. The
        adaptor DNA was purified and size-selected for a 9.5 to
        10.5 kb range using preparative agarose gel
        electrophoresis. Vector DNA was prepared from a derivative
        of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
        inducible derivative of plasmid R1. The vector was ligated
        with adaptors complementary to the insert adaptors and
        purified. The sheared, adaptor mouse DNA was annealed to
        adaptor vector DNA, and transformed into
        chemically-competent E. coli XL10-Gold (Stratagene) cells
        and selected for ampicillin resistance."

```


Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0054 row: A column: 13
 Seq primer: CACACAGAAACACGCTATGACC
 Class: plasmid ends
 High quality sequence stop: 23.
 Location/Qualifiers

FEATURES

source

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1..23
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0054A13"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, TI-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (GI|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

```

ORIGIN

```

Query Match      50.0%; Score 12; DB 11; Length 23;
Best Local Similarity 50.0%; Pred. No. 1.4e+06;
Matches 6; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 1 UAUUGUCUCUCC 12
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Db 11 TATTGTCCTCC 22

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RESULT 9

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AZ514958
LOCUS      1M0054A13F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
DEFINITION clone UUGC1M0054A13 F, genomic survey sequence.
ACCESSION  AZ514958
VERSION     AZ514958.1 GI:10696274
KEYWORDS   GSS.
SOURCE     Mus musculus (house mouse)
ORGANISM   Mus musculus
            Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muridea; Muridae; Murinae; Mus.
            1 (bases 1 to 23)
            Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
            Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
            Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
            Niederhausern, A. and Wright, D., Weiss, R.
TITLE      Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
JOURNAL    Unpublished (2000)
COMMENT    Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA

```

Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0054 row: A column: 13
 Seq primer: CGTTGTAAACGACGCGCCAGT
 Class: plasmid ends
 High quality sequence stop: 23.
 Location/Qualifiers

FEATURES

source

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1..23
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0054A13"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, TI-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (GI|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

```

ORIGIN

```

Query Match      50.0%; Score 12; DB 11; Length 23;
Best Local Similarity 50.0%; Pred. No. 1.4e+06;
Matches 6; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 1 UAUUGUCUCUCC 12
   |:|:|:|:|
Db 11 TATTGTCCTCC 22

```

RESULT 10

```

CL983109/c
LOCUS      GC0348 TIGEM gene trap library Mus musculus cDNA clone 10863.13,
DEFINITION mRNA sequence.
ACCESSION  CL983109
VERSION     CL983109.1 GI:52420701
KEYWORDS   GSS.
SOURCE     Mus musculus (house mouse)
ORGANISM   Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muridea; Muridae; Murinae; Mus.
            1 (bases 1 to 27)
            Cobellis, G., Niclaus, G., Iovino, M., Romito, A., Marra, E.,
            Barbarisi, M., Sardiello, M., Di Giorgio, F.P., Iovino, N., Zollo, M.,
            Ballabio, A. and Cortese, R.
TITLE      Tagging genes with cassette-exchange sites
JOURNAL    Nucleic Acids Res. 33 (4), e44 (2005)
COMMENT    15741177
            Contact: TIGEM
            107
            TIGEM
            Via P. Castellino, 111, 80131 NAPOLI, ITALY
            Tel: +390816132205

```

Fax: +390815790919
 Email: cobelli@tigem.it
 Sequence tag generated by 5' RACE of total RNA from gene trap ES cell line. ES cell lines harboring insertion mutation of target gene are available upon request from TIGEM. Annotation information available from TIGEM
 Class: Gene Trap.

FEATURES

source
 1. .27
 /organism="Mus musculus"
 /mol_type="mRNA"
 /strain="129 ola"
 /db_xref="taxon:10090"
 /clone="10863.13"
 /sex="male"
 /cell_type="Embryonic stem cell"
 /cell_line="E14"
 /clone_lib="TIGEM gene trap library"
 /note="Vector: pFLIP1"

ORIGIN

Query Match 50.0%; Score 12; DB 13; Length 27;
 Best Local Similarity 55.0%; Pred. No. 1.4e+06;
 Matches 11; Conservative 4; Mismatches 5; Indels 0; Gaps 0;
 QY 5 GUCUCUCCUUCGCCACCUC 24
 | : : : : :
 DB 23 GGCTCTCACTCCGCCAGCTC 4

RESULT 11

BH901484
 LOCUS 28 bp DNA linear GSS 04-SEP-2002
 DEFINITION SALK_079650.53.10.x Arabidopsis thaliana TDNA insertion lines
 Arabidopsis thaliana genomic clone SALK_079650.53.10.x, genomic survey sequence.

ACCESSION BH901484.1 GI:22712365
 VERSION
 KEYWORDS
 SOURCE Arabidopsis thaliana (thale cress)

ORGANISM

Arabidopsis thaliana
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi.

1 (bases 1 to 28)

REFERENCE
 AUTHORS Alonso,J.M., Leisec,T.J., Barajas,P., Chen,H., Cheuk,R., Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L., Shinn,P., Zimmerman,J. and Ecker,J.R.

TITLE A Sequence-Indexed Library of Insertion Mutations in the

Arabidopsis Genome

Unpublished (2001)

Contact: Joseph R. Ecker

Salk Institute Genomic Analysis Laboratory (SIGNAL)

The Salk Institute for Biological Studies

10010 N. Torrey Pines Road, La Jolla, CA 92037, USA

Tel: 858 453 4100 x1752

Fax: 858 558 6379

Email: ecker@salk.edu

This is single pass sequence recovered from the left border of TDNA.

Class: TDNA tagged.

FEATURES

source
 1. .28
 /organism="Arabidopsis thaliana"
 /mol_type="genomic DNA"
 /ecotype="Col-0"
 /db_xref="taxon:3702"
 /clone="SALK_079650.53.10.x"

/clone_lib="Arabidopsis thaliana TDNA insertion lines"
 /notes="PCR was performed on Arabidopsis thaliana lines each of which contains one or more TDNA insertion elements. The resultant fragment for each line was directly sequenced to determine the genomic sequence at

the site of insertion. Details of the protocols used can be found at http://signal.salk.edu/tdna_protocols.html"

ORIGIN

Query Match 50.0%; Score 12; DB 11; Length 28;
 Best Local Similarity 40.0%; Pred. No. 1.4e+06;
 Matches 8; Conservative 7; Mismatches 5; Indels 0; Gaps 0;

QY 1 UAUUGUCUCCUUCGCCCA 20
 | : : : : :
 DB 5 TTTTCTCTCCCTGCACCA 24

RESULT 12

DME545811/c
 LOCUS 28 bp DNA linear GSS 24-FEB-2003
 DEFINITION Drosophila melanogaster flanking sequence of RS P element insertion
 P{RS3}CB-6297-3, clone library P{RS3}, genomic survey sequence.

ACCESSION AJ545811

VERSION AJ545811.1 GI:28553693

KEYWORDS GSS; genome survey sequence.

SOURCE Drosophila melanogaster (fruit fly)

ORGANISM

Drosophila melanogaster

Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

Ephydroidea; Drosophilidae; Drosophila.

REFERENCE

1 Ryder,E.J., Ashburner,M., Bagunya,J., Blows,F., Bucheton,A.,

Coulson,D., Dickson,B., Drummond,J., Glover,D., Guntton,N.,

Hafen,E., Hall,S., Heisenberg,M., Lepesant,J.A., Maroy,P.,

Mechler,B., O'Kane,C., Pflugfelder,G., Rasmuson-Lestander,A.,

Reuter,G., Roote,J., Szidonya,J., Wang,S., Webster,J. and

Russell,S.

Mapping of RS P element insertions in Drosophila melanogaster for

the DrosDel second generation deficiency kit

Unpublished

2 (bases 1 to 28)

REFERENCE Ryder,E.J.

Direct Submission

Submitted (17-FEB-2003) Ryder E.J., Department of Genetics,

University of Cambridge, Downing Street, CB2 3EH, UNITED KINGDOM

The insertion point of the P element is before base 1 of the

sequence. Further information about this P element insertion line

can be found at <http://www.flyseq.org.uk> and

<http://www.drosdel.org.uk>

FEATURES

source

1. .28

/organism="Drosophila melanogaster"

/mol_type="genomic DNA"

/db_xref="taxon:7227"

/chromosomes="3L"

/clone="P{RS3}CB-6297-3"

/clone_lib="P{RS3}"

/note="read=5' end"

misc_feature 1. .28

/note="P element insertion in the 5' to 3' orientation"

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QY 7 CUCUCCUUCGCCAC 21

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 DB 25 CTCTCTCTTCGCCAC 11

RESULT 13

AZ475883/c
 LOCUS 21 bp DNA linear GSS 04-OCT-2000
 DEFINITION IM0294J14F Mouse 10kb plasmid UUGc1M library Mus musculus genomic

clone UUGC1M0294J14 F, genomic survey sequence.

ACCESSION AZ475883

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VERSION AZ475883.1 GI:10634008
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 21)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmood,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
JOURNAL Contact: Robert B. Weiss
COMMENT University of Utah
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
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Seq primer: CGTTGTAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 21.

FEATURES source
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/sex="Male"
/lab_host="E. Coli strain XL10-Gold, TI-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptor DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (GI|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptor mouse DNA was annealed to
adaptor vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

ORIGIN
Query Match 48.3%; Score 11.6; DB 11; Length 21;
Best Local Similarity 44.4%; Pred. No. 2e+06;
Matches 8; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

QY 7 CUUCUCCUUGCCACCCU 24
Db 21 CTTCTCTTTCTCCCTTC 4

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DEFINITION similar to TR:Q40726 Q40726 DNA BINDING PROTEIN ;, mRNA sequence.

ACCESSION A1539240
VERSION A1539240.1 GI:4453375
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominiidae; Homo.
1 (bases 1 to 25)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
JOURNAL Contact: Robert Strausberg, Ph.D.
COMMENT Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html

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High quality sequence stop: 1
POLYA=No.

FEATURES source
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/clone_lib="NCI CGAP Ut3"
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Site 2: NotI; Cloned unidirectionally. Primer: Oligo dt.
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Query Match 48.3%; Score 11.6; DB 1; Length 25;
Best Local Similarity 44.4%; Pred. No. 2e+06;
Matches 8; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

QY 6 UCUCUCCUUGCCACCCU 23
Db 25 TTTCCCTTTCCTCCTCT 8

RESULT 15
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LOCUS clone UUGC1M0256G18 F, genomic survey sequence.
DEFINITION AZ454352
ACCESSION AZ454352.1 GI:10612477
VERSION AZ454352.1
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 26)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmood,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb

```

**JOURNAL
COMMENT**

plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah
Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
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Plate: 0256 row: G column: 18
Seq primer: CGTTGTAAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 26.

FEATURES

source

ORIGIN

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Query Match      48.3%; Score 11.6; DB 11; Length 26;
Best Local Similarity 50.0%; Pred. No. 2.1e+06;
Matches 9; Conservative 5; Mismatches 4; Indels 0; Caps 0;
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Search completed: October 16, 2006, 15:51:29
Job time : 1035.18 secs

GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 16, 2006, 14:11:03 ; Search time 55.5789 Seconds
(without alignments)
807.979 Million cell updates/sec

Title: US-10-604-726A-5136
Perfect score: 24
Sequence: 1 uauugucuccuucgcaccuc 24

Scoring table: IDENTITY NUC
Gapop 10_0 , Gapext 1.0

Searched: 1403666 seqs, 935554401 residues

Total number of hits satisfying chosen parameters: 1097684

Minimum DB seq length: 0
Maximum DB seq length: 30

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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C 2	15.6	65.0	24	2	US-08-014-943A-15
C 3	15.6	65.0	24	2	US-08-486-421-20
C 4	15.6	65.0	24	2	US-08-486-421-38
C 5	15.6	65.0	24	2	US-08-470-911-20
C 6	15.6	65.0	24	2	US-08-470-911-38
C 7	15.6	65.0	24	2	US-08-486-809-20
C 8	15.6	65.0	24	2	US-08-486-809-38
C 9	14.8	61.7	29	3	US-07-672-530C-16
C 10	14.4	60.0	18	2	US-07-977-284A-99
C 11	14.4	60.0	18	2	US-08-256-426B-99
C 12	14.2	59.2	21	2	US-08-242-664-38
C 13	14.2	59.2	21	2	US-08-484-138-38
C 14	14.2	59.2	21	7	PCT-US95-06379-38
C 15	14	58.3	24	2	US-08-014-943A-12
C 16	14	58.3	24	2	US-08-486-421-34
C 17	14	58.3	24	2	US-08-470-911-34
C 18	14	58.3	24	2	US-08-486-809-34
C 19	14	58.3	25	3	US-09-396-196G-81941
C 20	13.8	57.5	20	3	US-09-118-408-10
C 21	13.8	57.5	20	3	US-09-506-855-10
C 22	13.8	57.5	20	3	US-09-311-178B-10
C 23	13.8	57.5	20	3	US-09-619-740-10

C 24	13.8	57.5	20	3	US-09-198-452A-3360	Sequence 3360, Ap
C 25	13.8	57.5	20	3	US-09-506-852-10	Sequence 10, Appl
C 26	13.8	57.5	20	3	US-10-392-706-10	Sequence 10, Appl
C 27	13.6	56.7	25	3	US-09-396-196G-64399	Sequence 64399, A
C 28	13.6	56.7	25	3	US-09-396-196G-119671	Sequence 119671, A
C 29	13.4	55.8	17	2	US-07-977-284A-100	Sequence 100, App
C 30	13.4	55.8	17	2	US-08-256-426B-100	Sequence 100, App
C 31	13.4	55.8	24	3	US-08-445-463B-56	Sequence 56, Appl
C 32	13.4	55.8	24	3	US-08-445-463B-57	Sequence 56, Appl
C 33	13.4	55.8	24	3	US-08-445-464C-56	Sequence 57, Appl
C 34	13.4	55.8	24	3	US-08-445-464C-57	Sequence 57, Appl
C 35	13.4	55.8	24	3	US-08-044-857D-56	Sequence 56, Appl
C 36	13.4	55.8	24	3	US-08-044-857D-57	Sequence 57, Appl
C 37	13.4	55.8	24	7	PCT-US94-03437-56	Sequence 56, Appl
C 38	13.4	55.8	24	7	PCT-US94-03437-57	Sequence 57, Appl
C 39	13.4	55.8	25	3	US-09-543-398B-365	Sequence 365, App
C 40	13.4	55.8	25	3	US-09-543-398B-365	Sequence 365, App
C 41	13.4	55.8	25	3	US-09-396-196G-14417	Sequence 14417, A
C 42	13.4	55.8	25	3	US-09-396-196G-14428	Sequence 14428, A
C 43	13.4	55.8	25	3	US-09-396-196G-57430	Sequence 57430, A
C 44	13.4	55.8	25	3	US-09-396-196G-117149	Sequence 117149, A
C 45	13.4	55.8	28	3	US-09-175-928-59	Sequence 59, Appl

ALIGNMENTS

RESULT 1
US-08-014-943A-3/c
; Sequence 3, Application US/08014943A
; Patent No. 5545551
; GENERAL INFORMATION:
; APPLICANT: Johnson, Edward M.
; APPLICANT: Bergmann, Andrew D.
; TITLE OF INVENTION: Cloning And Expression Of PUR Protein
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/014,943A
; FILING DATE: 02/FEB/1992
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 6923-033
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212 790-9090
; TELEFAX: 212 869-8864/9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 24 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: DNA (genomic)
US-08-014-943A-3

Query Match 65.0%; Score 15.6; DB 2; Length 24;
Best Local Similarity 50.0%; Pred. No. 6.4e+02;
Matches 11; Conservative 7; Mismatches 4; Indels 0; Gaps 0;

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Db 23 TTTTCTCTCCCTCCACCACCTC 2

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RESULT 2
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; Sequence 15, Application US/08014943A
; Patent No. 5545551
; GENERAL INFORMATION:
; APPLICANT: Johnson, Edward M.
; APPLICANT: Bergemann, Andrew D.
; TITLE OF INVENTION: Cloning And Expression Of PUR Protein
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/014,943A
; FILING DATE: 02/FEB/1992
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 6923-033
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212 790-9090
; TELEFAX: 212 869-8864/9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 24 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: DNA (genomic)
US-08-014-943A-15

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RECORD 3
 US-08-486-421-20/c
 ; Sequence 20, Application US/08486421
 ; Patent No. 5672479
 ; GENERAL INFORMATION:
 ; APPLICANT: Johnson, Edward M.
 ; APPLICANT: Bergemann, Andrew D.
 ; TITLE OF INVENTION: CLONING AND EXPRESSION OF PUR PROTEIN
 ; NUMBER OF SEQUENCES: 51
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Pennie & Edmonds
 ; STREET: 1155 Avenue of the Americas
 ; CITY: New York
 ; STATE: New York
 ; COUNTRY: U.S.A.
 ; ZIP: 10036-2711
 ; COMPUTER READABLE FORM:

RESULT 4
US-08-486-421-38
; Sequence 38, Application US/08486421
; Patent No. 5672479
; GENERAL INFORMATION:
; APPLICANT: Johnson, Edward M.
; APPLICANT: Bergemann, Andrew D.
; TITLE OF INVENTION: CLONING AND EXPRESSION OF PUR PROTEIN
; NUMBER OF SEQUENCES: 51
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/486.421
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/470,911
; FILING DATE: 06-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 6923-053
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEEX: 66141 PENNIE

RESULT 4
US-08-486-421-38
; Sequence 38, Application US/08486421
; Patent No. 5672479
; GENERAL INFORMATION:
; APPLICANT: Johnson, Edward M.
; APPLICANT: Bergemann, Andrew D.
; TITLE OF INVENTION: CLONING AND EXPRESSION OF PUR PROTEIN
; NUMBER OF SEQUENCES: 51
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/486.421
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/470,911
; FILING DATE: 06-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 6923-053
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEEX: 66141 PENNIE

; INFORMATION FOR SEQ ID NO: 38:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 24 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-486-421-38

Query Match 65.0%; Score 15.6; DB 2; Length 24;
Best Local Similarity 50.0%; Pred. No. 6.4e+02;
Matches 11; Conservative 7; Mismatches 4; Indels 0; Gaps 0;

QY 3 UUGUCUCUCCUUGCCACCUC 24
Db 2 TTTTCTCTCCTCCACCACCTC 23

RESULT 5

US-08-470-911-20/c
; Sequence 20, Application US/08470911
; Patent No. 5756684
; GENERAL INFORMATION:
; APPLICANT: Johnson, Edward M.
; APPLICANT: Bergemann, Andrew D.
; TITLE OF INVENTION: CLONING AND EXPRESSION OF PUR PROTEIN
; NUMBER OF SEQUENCES: 51
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/470,911
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 6923-053
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; INFORMATION FOR SEQ ID NO: 20:
; LENGTH: 24 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: DNA (genomic)
US-08-470-911-20

Query Match 65.0%; Score 15.6; DB 2; Length 24;
Best Local Similarity 50.0%; Pred. No. 6.4e+02;
Matches 11; Conservative 7; Mismatches 4; Indels 0; Gaps 0;

QY 3 UUGUCUCUCCUUGCCACCUC 24
Db 23 TTTTCTCTCCTCCACCACCTC 2

RESULT 6

US-08-470-911-38
; Sequence 38, Application US/08470911
; Patent No. 5756684

; GENERAL INFORMATION:
; APPLICANT: Johnson, Edward M.
; APPLICANT: Bergemann, Andrew D.
; TITLE OF INVENTION: CLONING AND EXPRESSION OF PUR PROTEIN
; NUMBER OF SEQUENCES: 51
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/470,911
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 6923-053
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 38:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 24 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-470-911-38

Query Match 65.0%; Score 15.6; DB 2; Length 24;
Best Local Similarity 50.0%; Pred. No. 6.4e+02;
Matches 11; Conservative 7; Mismatches 4; Indels 0; Gaps 0;

QY 3 UUGUCUCUCCUUGCCACCUC 24
Db 2 TTTTCTCTCCTCCACCACCTC 23

RESULT 7

US-08-486-809-20/c
; Sequence 20, Application US/08486809
; Patent No. 5869622
; GENERAL INFORMATION:
; APPLICANT: Johnson, Edward M.
; APPLICANT: Bergemann, Andrew D.
; TITLE OF INVENTION: CLONING AND EXPRESSION OF PUR PROTEIN
; NUMBER OF SEQUENCES: 51
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/486,809
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:

```
/ APPLICATION NUMBER: US 08/470,911
/ FILING DATE: 06-JUN-1995
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Coruzzi, Laura A.
/ REGISTRATION NUMBER: 30,742
/ REFERENCE/DOCKET NUMBER: 6923-053
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (212) 790-9090
/ TELEFAX: (212) 869-9741/8864
/ TELEX: 66141 PENNIE
/ INFORMATION FOR SEQ ID NO: 20:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 24 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: unknown
/ MOLECULE TYPE: DNA (genomic)
US-08-486-809-20

Query Match 65.0%; Score 15.6; DB 2; Length 24;
Best Local Similarity 50.0%; Pred. No. 6.4e+02;
Matches 11; Conservative 7; Mismatches 4; Indels 0; Gaps 0;

QY 3 UUGUCUCUCUUCGCGCACCC 24
Db 23 TTTTCTCTCCTCCACCACTC 2

RESULT 8
US-08-486-809-38
/ Sequence 38, Application US/08486809
/ Patent No. 5869622
/ GENERAL INFORMATION:
/ APPLICANT: Johnson, Edward M.
/ APPLICANT: Bergemann, Andrew D.
/ TITLE OF INVENTION: CLONING AND EXPRESSION OF PUR PROTEIN
/ NUMBER OF SEQUENCES: 51
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Pennie & Edmonds
/ STREET: 1155 Avenue of the Americas
/ CITY: New York
/ STATE: New York
/ COUNTRY: U.S.A.
/ ZIP: 10036-2711
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/486,809
/ FILING DATE: 07-JUN-1995
/ CLASSIFICATION: 435
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/470,911
/ FILING DATE: 06-JUN-1995
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Coruzzi, Laura A.
/ REGISTRATION NUMBER: 30,742
/ REFERENCE/DOCKET NUMBER: 6923-053
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (212) 790-9090
/ TELEFAX: (212) 869-9741/8864
/ TELEX: 66141 PENNIE
/ INFORMATION FOR SEQ ID NO: 38:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 24 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: DNA
US-08-486-809-38
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Query Match 65.0%; Score 15.6; DB 2; Length 24;
Best Local Similarity 50.0%; Pred. No. 6.4e+02;
Matches 11; Conservative 7; Mismatches 4; Indels 0; Gaps 0;

QY 3 UUGUCUCUCUUCGCGCACCC 24
Db 2 TTTTCTCTCCTCCACCACTC 23

RESULT 9
US-07-672-530C-16/c
/ Sequence 16, Application US/07672530C
/ Patent No. 6492137
/ GENERAL INFORMATION:
/ APPLICANT: SUCOV, HENRY M
/ APPLICANT: EVANS, RONALD M
/ APPLICANT: UMESONO, KAZUHIKO
/ TITLE OF INVENTION: RESPONSE ELEMENT COMPOSITIONS AND ASSAYS EMPLOYING SAME
/ FILE REFERENCE: 088802/1552
/ CURRENT APPLICATION NUMBER: US/07/672,530C
/ CURRENT FILING DATE: 1991-03-19
/ PRIOR APPLICATION NUMBER: 07/438,757
/ PRIOR FILING DATE: 1989-11-16
/ NUMBER OF SEQ ID NOS: 51
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 16
/ LENGTH: 29
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence:
/ OTHER INFORMATION: Oligonucleotide, M2
US-07-672-530C-16

Query Match 61.7%; Score 14.8; DB 3; Length 29;
Best Local Similarity 55.6%; Pred. No. 1.5e+03;
Matches 10; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

QY 7 CUCUCUUCGCGCACCC 24
Db 23 CTGCTCTTCGTCACCTC 6

RESULT 10
US-07-977-284A-99
/ Sequence 99, Application US/07977284A
/ Patent No. 5558988
/ GENERAL INFORMATION:
/ APPLICANT: Prockop, Darwin J.
/ APPLICANT: Ala-Kokko, Leena
/ APPLICANT: Williams, Charlene J.
/ APPLICANT: Rytvanieni, Pertti
/ APPLICANT: Baldwin, Clinton
/ APPLICANT: Hopkinson, Ian
/ APPLICANT: Ahmad, Nilofer Nina
/ TITLE OF INVENTION: METHODS OF DETECTING A GENETIC
/ TITLE OF INVENTION: PREDISPOSITION FOR OSTEOARTHRITIS
/ NUMBER OF SEQUENCES: 261
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Woodcock, Waehburn, Kurtz, Mackiewicz & No. 5558988ris
/ STREET: One Liberty Place, 46th floor
/ CITY: Philadelphia
/ STATE: PA
/ COUNTRY: USA
/ ZIP: 19103
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: WordPerfect 5.1
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/07/977,284A
/ FILING DATE: 13-NOV-1992
```



```
/ CLASSIFICATION: 435
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER:
/ FILING DATE:
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Deluca, Mark
/ REGISTRATION NUMBER: 33,229
/ REFERENCE/DOCKET NUMBER: TJU-0697
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (215) 568-3100
/ TELEFAX: (215) 568-3439
/ INFORMATION FOR SEQ ID NO: 99:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 18
/ TYPE: NUCLEIC ACID
/ STRANDEDNESS: SINGLE
/ TOPOLOGY: LINEAR
/ ANTI-SENSE: NO
/ US-07-977-284A-99

Query Match 60.0%; Score 14.4; DB 2; Length 18;
Best Local Similarity 62.5%; Pred. No. 2.1e+03;
Matches 10; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 9 CUCCUUUCCGACCUC 24
Db 3 CTCCTTTCCACCTC 18

RESULT 11
US-08-256-426B-99
; Sequence 99, Application US/08256426B
; Patent No. 5948611
; GENERAL INFORMATION:
; APPLICANT: Prockop, Darwin J.
; APPLICANT: Ala-Kokko, Leena
; APPLICANT: Williams, Charlene J.
; APPLICANT: Ritvaniemi, Pertti
; APPLICANT: Baldwin, Clinton
; APPLICANT: Hopkinson, Ian
; APPLICANT: Ahmad, Nilofer Nina
; TITLE OF INVENTION: Methods of Detecting A Genetic
; NUMBER OF SEQUENCES: 293
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5948611ris
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: DISKETTE, 3.5 INCH
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows 3.1
; SOFTWARE: WORDPERFECT 6.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/256,426B
; FILING DATE: 03-FEB-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/10964
; FILING DATE: 12-NOV-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/977,284
; FILING DATE: 13-NOV-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Mark Deluca
; REGISTRATION NUMBER: 33,229
; REFERENCE/DOCKET NUMBER: TJU-1082
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-3100
; TELEFAX: (215) 568-3439
; INFORMATION FOR SEQ ID NO: 99:

/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 18
/ TYPE: NUCLEIC ACID
/ STRANDEDNESS: SINGLE
/ TOPOLOGY: LINEAR
/ ANTI-SENSE: NO
/ US-08-256-426B-99

Query Match 60.0%; Score 14.4; DB 2; Length 18;
Best Local Similarity 62.5%; Pred. No. 2.1e+03;
Matches 10; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 9 CUCCUUUCCGACCUC 24
Db 3 CTCCTTTCCACCTC 18

RESULT 12
US-08-242-664-38/c
; Sequence 38, Application US/08242664
; Patent No. 5571937
; GENERAL INFORMATION:
; APPLICANT: Watanabe, Kyoichi A.
; APPLICANT: Ren, Wu-Yun
; APPLICANT: Well, Roger
; TITLE OF INVENTION: Complementary DNA and Toxins
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham
; STREET: 30 Rockefeller Plaza
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10112
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch 1.44Mb
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/242,664
; FILING DATE: May 12, 1994
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 44683
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-977-9550
; TELEFAX: 212-664-0525
; INFORMATION FOR SEQ ID NO: 38:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-242-664-38

Query Match 59.2%; Score 14.2; DB 2; Length 21;
Best Local Similarity 36.8%; Pred. No. 2.7e+03;
Matches 7; Conservative 9; Mismatches 3; Indels 0; Gaps 0;

QY 1 UAUUGUCUCUCCUUGGCC 19
Db 19 TTTTATCTCTCCTTTCTCC 1

RESULT 13
US-08-484-138-38/c
; Sequence 38, Application US/08484138
; Patent No. 5652350
; GENERAL INFORMATION:
```

APPLICANT: Watanabe, Kyoichi A.
APPLICANT: Ren, Wu-Yun
APPLICANT: Weil, Roger
TITLE OF INVENTION: Complementary DNA and Toxins
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper & Dunham LLP
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch 1.44MB
COMPUTER: IBM PC
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,138
FILING DATE: June 7, 1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 44683-Z/JPW/MJG
TELEPHONE: 212-977-9550
TELEFAX: 212-664-0525
INFORMATION FOR SEQ ID NO: 38:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-484-138-38

Query Match 59.2%; Score 14.2; DB 2; Length 21;
Best Local Similarity 36.8%; Pred. No. 2.7e+03;
Matches 7; Conservative 9; Mismatches 3; Indels 0; Gaps 0;

QY 1 UAUUGUCUCUCCUUGGCC 19
Db 19 TTTTATCTCTCCTTTCTCC 1

RESULT 14
PCT-US95-06379-38/c
Sequence 38, Application PC/TUS9506379
GENERAL INFORMATION:
APPLICANT: Watanabe, Kyoichi A.
APPLICANT: Ren, Wu-Yun
APPLICANT: Weil, Roger
TITLE OF INVENTION: Complementary DNA and Toxins
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper & Dunham LLP
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch 1.44MB
COMPUTER: IBM PC
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/06379
FILING DATE: May 13, 1994
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.

REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 44683-PCT
TELEPHONE: 212-278-0400
TELEFAX: 212-391-0526
INFORMATION FOR SEQ ID NO: 38:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
PCT-US95-06379-38

Query Match 59.2%; Score 14.2; DB 7; Length 21;
Best Local Similarity 36.8%; Pred. No. 2.7e+03;
Matches 7; Conservative 9; Mismatches 3; Indels 0; Gaps 0;

QY 1 UAUUGUCUCUCCUUGGCC 19
Db 19 TTTTATCTCTCCTTTCTCC 1

RESULT 15
US-08-014-943A-12/c
Sequence 12, Application US/08014943A
Patent No. 5545551
GENERAL INFORMATION:
APPLICANT: Johnson, Edward M.
APPLICANT: Bergemann, Andrew D.
TITLE OF INVENTION: Cloning And Expression Of PUR Protein
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/014,943A
FILING DATE: 02/FEB/1992
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 6923-033
TELEPHONE: 212 790-9090
TELEFAX: 212 869-8864/9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 24 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
US-08-014-943A-12

Query Match 58.3%; Score 14; DB 2; Length 24;
Best Local Similarity 40.9%; Pred. No. 3.4e+03;
Matches 9; Conservative 8; Mismatches 5; Indels 0; Gaps 0;

QY 3 UUGUCUCUCCUUGGCCACCUC 24
Db 23 TTTTCTCTTTTCCACCACCTC 2

Search completed: October 16, 2006, 14:47:14
Job time : 56.5789 secs

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Result No.	Score	Query		Length	DB	ID	Description
		Match	%				
C 1	16.2	67.5	25	16	US-11-136-527-336045	Sequence 336045	
C 2	16	66.7	25	9	US-10-719-900-980988	Sequence 980988	
C 3	16	66.7	25	10	US-10-956-157-42579	Sequence 42579	
C 4	16	66.7	25	10	US-10-956-157-88871	Sequence 88871	
C 5	16	66.7	25	10	US-10-956-157-88877	Sequence 88877	
C 6	16	66.7	25	13	US-11-060-756-47774	Sequence 47774	
C 7	16	66.7	25	13	US-11-060-756-47788	Sequence 47788	
C 8	15.8	65.8	24	11	US-10-310-9148-205339	Sequence 205339	
C 9	15.8	65.8	25	16	US-11-136-527-276878	Sequence 276878	
C 10	15.8	65.8	25	16	US-11-136-527-276903	Sequence 276903	
C 11	15.6	65.0	25	9	US-10-719-900-678730	Sequence 678730	
C 12	15.6	65.0	25	13	US-11-036-317-35946	Sequence 35946	
C 13	15.4	64.2	20	11	US-10-310-9148-498782	Sequence 498782	
C 14	15.4	64.2	20	11	US-10-956-157-21624	Sequence 21624	
C 15	15.4	64.2	25	10	US-10-956-157-21630	Sequence 21630	
C 16	15.4	64.2	25	10	US-10-956-157-21634	Sequence 21634	
C 17	15.4	64.2	25	10	US-10-956-157-21637	Sequence 21637	

ALIGNMENTS

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RESULT 1
US-11-136-527-336045/c
; Sequence 336045, Application US/11136527
; Publication No. US20050287570A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
; FILE REFERENCE: 031896-041000 (AM101086)
; CURRENT APPLICATION NUMBER: US/11/136,527
; CURRENT FILING DATE: 2005-05-25
; PRIOR APPLICATION NUMBER: US 60/574,294
; PRIOR FILING DATE: 2005-05-26
; NUMBER OF SEQ ID NOS: 362830
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 336045
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Probe
US-11-136-527-336045

Query Match      67.5%; Score 16.2; DB 16; Length 25;
Best Local Similarity 52.4%; Pred. No. 3.7e+03;
Matches 11; Conservative 7; Mismatches 3; Indels 0; Gaps 0;

QY      2 AUGUGUCUCUCUUCGCCACC 22
Db      25 ATTGCTTTCCGTTGCCACC 5
      ||::||::||::|||
      |::|::|::|::|

RESULT 2
US-10-719-900-980988
; Sequence 980988, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
```



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; FILE REFERENCE: AM101083 (031896-042000)
; CURRENT APPLICATION NUMBER: US/11/060,756
; CURRENT FILING DATE: 2005-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 47788
; LENGTH: 25
; TYPE: DNA
; ORGANISM: probe
US-11-060-756-47788

Query Match          66.7%; Score 16; DB 13; Length 25;
Best Local Similarity 45.8%; Pred.No. 4.5e+03;
Matches 11; Conservative 8; Mismatches 5; Indels 0; Gaps 0;

QY      1 UAUGUCUCUCCUUUUGCGCACCU 24
       :|: |:||::|||:|
Db       25 TATCTTCCTCTTCTCCACATC 2

RESULT 8
US-10-310-914A-205339
; Sequence 205339, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 205339
; LENGTH: 24
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-205339

Query Match          65.8%; Score 15.8; DB 11; Length 24;
Best Local Similarity 89.5%; Pred.No. 5.5e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      2 AUGGUCUCUCCUUUUGCGCA 20
       |||||||
Db       5 AUGGUCUCUCCUUUCCCCA 23

RESULT 9
US-11-136-527-276878
; Sequence 276878, Application US/11136527
; Publication No. US20050287570A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
; FILE REFERENCE: 031896-041000 (AM101086)
; CURRENT APPLICATION NUMBER: US/11/136,527
; CURRENT FILING DATE: 2005-05-25
; PRIOR APPLICATION NUMBER: US 60/574,294
; PRIOR FILING DATE: 2005-05-26
; NUMBER OF SEQ ID NOS: 362830
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 276878
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Probe
US-11-136-527-276878

Query Match          65.8%; Score 15.8; DB 16; Length 25;
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; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 35846
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-35846

Query Match      65.0%; Score 15.6; DB 13; Length 25;
Best Local Similarity 40.9%; Pred.No.6.7e+03;
Matches 9; Conservative 9; Mismatches 4; Indels 0; Gaps 0;

QY    2 AUGUCUCUCUCCUUGCGCACCU 23
      ||:::||::||::||::||::|
Db     2 ATTCTGTCTCCTTGGCTACTT 23

RESULT 13
US-10-310-914A-498782
; Sequence 498782, Application US/10310914A
; Publication No. US20080003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvatrat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 498782
; LENGTH: 20
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-498782

Query Match      64.2%; Score 15.4; DB 11; Length 20;
Best Local Similarity 94.1%; Pred.No.8.1e+03;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY    6 UCUCUCCUUUCGCCACC 22
      |||||||||||||
Db     3 UCUCUCCUUUCGCCCCC 19

RESULT 14
US-10-956-157-21624/c
; Sequence 21624, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 21624
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
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1	14.6	60.8	25	8	US-11-217-529-33285	Sequence 33285, A
2	14.2	59.2	25	8	US-11-217-529-35946	Sequence 35946, A
C 3	14.2	59.2	25	8	US-11-217-529-171625	Sequence 171625, S
	14.2	59.2	25	9	US-11-348-413-247872	Sequence 247872, C
4	14.2	59.2	25	9	US-11-348-413-247873	Sequence 247873, S
5	14.2	59.2	25	9	US-11-348-413-247874	Sequence 247874, C
6	14.2	59.2	25	9	US-11-348-413-247875	Sequence 247875, S
7	14.2	59.2	25	9	US-11-348-413-247876	Sequence 247876, C
8	14.2	59.2	25	9	US-11-348-413-485166	Sequence 485166, S
9	14.2	59.2	25	9	US-11-348-413-485167	Sequence 485167, C
10	14.2	59.2	25	9	US-11-348-413-485168	Sequence 485168, S
11	14.2	59.2	25	9	US-11-348-413-485634	Sequence 485634, C
12	14.2	59.2	25	9	US-11-348-413-485635	Sequence 485635, S
13	14.2	59.2	25	9	US-11-348-413-689385	Sequence 689385, C
14	14.2	59.2	25	9	US-11-348-413-689385	Sequence 689385, S
15	14.2	59.2	25	9	US-11-348-413-861056	Sequence 861056, C
16	14.2	59.2	25	9	US-11-348-413-861057	Sequence 861057, S
17	14.2	59.2	25	9	US-11-348-413-861058	Sequence 861058, C
18	14.2	59.2	25	9	US-11-348-413-1129256	Sequence 1129256, S
19	14.2	59.2	25	9	US-11-348-413-1129777	Sequence 1129777, C
20	14	58.3	25	9	US-11-348-413-40425	Sequence 40425, A
21	14	58.3	25	9	US-11-348-413-40426	Sequence 40426, A
22	14	58.3	25	9	US-11-348-413-628721	Sequence 628721, S
23	14	58.3	25	9	US-11-348-413-848732	Sequence 848732, C

; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; PRIOR FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 35946
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-35946

Query Match 59.2%; Score 14.2; DB 8; Length 25;
Best Local Similarity 42.1%; Pred. No. 3.1e+03;
Matches 8; Conservative 8; Mismatches 3; Indels 0; Gaps 0;

QY 3 UUGUCUCUCUUCGCGCAC 21
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Db 4 TTGCTGTAATTTCGCCAC 22

RESULT 3

US-11-217-529-171625/c
; Sequence 171625, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; PRIOR FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 171625
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-171625

Query Match 59.2%; Score 14.2; DB 8; Length 25;
Best Local Similarity 47.4%; Pred. No. 3.1e+03;
Matches 9; Conservative 7; Mismatches 3; Indels 0; Gaps 0;

QY 1 UAUUGUCUCUCUUCGCC 19
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Db 21 TATCGTCTCTTTTCGCC 3

RESULT 4

US-11-348-413-247872/c
; Sequence 247872, Application US/11348413
; Publication No. US20060160121A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; APPLICANT: Murphy, Ellen
; APPLICANT: Olmsted, Stephen
; TITLE OF INVENTION: PROBE ARRAYS FOR DETECTING MULTIPLE STRAINS OF DIFFERENT SPECIES
; FILE REFERENCE: 031896-084100 (AM 101724)
; CURRENT APPLICATION NUMBER: US/11/348,413
; CURRENT FILING DATE: 2006-02-07
; PRIOR APPLICATION NUMBER: PCT/US05/035471
; PRIOR FILING DATE: 2005-10-05
; PRIOR APPLICATION NUMBER: US 11/243,445
; PRIOR FILING DATE: 2005-10-05

; PRIOR APPLICATION NUMBER: US 60/615,573
; PRIOR FILING DATE: 2004-10-05
; NUMBER OF SEQ ID NOS: 1276209
; SEQ ID NO 247872
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: probe
; NAME/KEY: misc.feature
; LOCATION: (1)..(25)
; OTHER INFORMATION: SEQ ID NO: 7205; WAN01UM2G; Start 113; Stop 137;
; OTHER INFORMATION: 000000001100000
US-11-348-413-247872

Query Match 59.2%; Score 14.2; DB 9; Length 25;
Best Local Similarity 47.4%; Pred. No. 3.1e+03;
Matches 9; Conservative 7; Mismatches 3; Indels 0; Gaps 0;

QY 2 AUUGUCUCUCUUCGCCA 20
 |:|::|::|::|
Db 25 ATAGTCTCTTTTAGCCA 7

RESULT 5

US-11-348-413-247873/c
; Sequence 247873, Application US/11348413
; Publication No. US20060160121A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; APPLICANT: Murphy, Ellen
; APPLICANT: Olmsted, Stephen
; TITLE OF INVENTION: PROBE ARRAYS FOR DETECTING MULTIPLE STRAINS OF DIFFERENT SPECIES
; FILE REFERENCE: 031896-084100 (AM 101724)
; CURRENT APPLICATION NUMBER: US/11/348,413
; CURRENT FILING DATE: 2006-02-07
; PRIOR APPLICATION NUMBER: PCT/US05/035471
; PRIOR FILING DATE: 2005-10-05
; PRIOR APPLICATION NUMBER: US 11/243,445
; PRIOR FILING DATE: 2005-10-05
; PRIOR APPLICATION NUMBER: US 60/615,573
; PRIOR FILING DATE: 2004-10-05
; NUMBER OF SEQ ID NOS: 1276209
; SEQ ID NO 247873
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: probe
; NAME/KEY: misc.feature
; LOCATION: (1)..(25)
; OTHER INFORMATION: SEQ ID NO: 7205; WAN01UM2G; Start 114; Stop 138;
; OTHER INFORMATION: 000000001100000
US-11-348-413-247873

Query Match 59.2%; Score 14.2; DB 9; Length 25;
Best Local Similarity 47.4%; Pred. No. 3.1e+03;
Matches 9; Conservative 7; Mismatches 3; Indels 0; Gaps 0;

QY 2 AUUGUCUCUCUUCGCCA 20
 |:|::|::|::|
Db 24 ATAGTCTCTTTTAGCCA 6

RESULT 6

US-11-348-413-247874/c
; Sequence 247874, Application US/11348413
; Publication No. US20060160121A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth

Query Match 59.2%; Score 14.2; DB 9; Length 25;
Best Local Similarity 47.4%; Pred. No. 3.1e+03;
Matches 9; Conservative 7; Mismatches 3; Indels 0; Gaps 0;

RESULT 9
US-11-348-413-485166/c
; Sequence 485166, Application US/11348413
; Publication No. US20060160121A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; APPLICANT: Murphy, Ellen
; APPLICANT: Olmsted., Stephen
; TITLE OF INVENTION: PROBE ARRAYS FOR DETECTING MULTIPLE STRAINS OF DIFFERENT SPECIES
; FILE REFERENCE: 031896-084100 (AM 101724)
; CURRENT APPLICATION NUMBER: US/11/348,413
; CURRENT FILING DATE: 2006-02-07
; PRIOR APPLICATION NUMBER: PCT/US05/035471
; PRIOR FILING DATE: 2005-10-05
; PRIOR APPLICATION NUMBER: US 11/243,445
; PRIOR FILING DATE: 2005-10-05
; PRIOR APPLICATION NUMBER: US 60/615,573
; PRIOR FILING DATE: 2004-10-05
; NUMBER OF SEQ ID NOS: 1276209
; SEQ ID NO 485166
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: probe

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; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(25)
; OTHER INFORMATION: SEQ ID NO: 14491; WAN01UQID; Start 1352; Stop 1376;
; NUMBER OF SEQ ID NOS: 00000000001000
; OTHER INFORMATION: 00000000001000
US-11-348-413-485166

Query Match          59.2%; Score 14.2; DB 9; Length 25;
Best Local Similarity 47.4%; Pred. No. 3.1e+03;
Matches 9; Conservative 7; Mismatches 3; Indels 0; Gaps 0;

QY 4 UGUCUCUCUUCGCCACC 22
Db 25 TGTCTTTCCTTTAACCACC 7

RESULT 10
US-11-348-413-485167/c
; Sequence 485167, Application US/11348413
; Publication No. US20060160121A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; APPLICANT: Murphy, Ellen
; APPLICANT: Olmsted, Stephen
; TITLE OF INVENTION: PROBE ARRAYS FOR DETECTING MULTIPLE STRAINS OF DIFFERENT SPECIES
; FILE REFERENCE: 031896-084100 (AM 101724)
; CURRENT APPLICATION NUMBER: US/11/348,413
; PRIOR FILING DATE: 2006-02-07
; PRIOR APPLICATION NUMBER: PCT/US05/035471
; PRIOR FILING DATE: 2005-10-05
; PRIOR APPLICATION NUMBER: US 11/243,445
; PRIOR FILING DATE: 2005-10-05
; PRIOR APPLICATION NUMBER: US 60/615,573
; PRIOR FILING DATE: 2004-10-05
; NUMBER OF SEQ ID NOS: 1276209
; SEQ ID NO 485167
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: probe
; NAME/KEY: misc feature
; LOCATION: (1)..(25)
; OTHER INFORMATION: SEQ ID NO: 14491; WAN01UQID; Start 1353; Stop 1377;
; OTHER INFORMATION: 00000000001000
US-11-348-413-485167

Query Match          59.2%; Score 14.2; DB 9; Length 25;
Best Local Similarity 47.4%; Pred. No. 3.1e+03;
Matches 9; Conservative 7; Mismatches 3; Indels 0; Gaps 0;

QY 4 UGUCUCUCUUCGCCACC 22
Db 24 TGTCTTTCCTTTAACCACC 6

RESULT 11
US-11-348-413-485168/c
; Sequence 485168, Application US/11348413
; Publication No. US20060160121A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; APPLICANT: Murphy, Ellen
; APPLICANT: Olmsted, Stephen
; TITLE OF INVENTION: PROBE ARRAYS FOR DETECTING MULTIPLE STRAINS OF DIFFERENT SPECIES
; FILE REFERENCE: 031896-084100 (AM 101724)
; CURRENT APPLICATION NUMBER: US/11/348,413
; PRIOR FILING DATE: 2006-02-07
; PRIOR APPLICATION NUMBER: PCT/US05/035471
; PRIOR FILING DATE: 2005-10-05
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; PRIOR APPLICATION NUMBER: US 11/243,445
; PRIOR FILING DATE: 2005-10-05
; PRIOR APPLICATION NUMBER: US 60/615,573
; PRIOR FILING DATE: 2004-10-05
; NUMBER OF SEQ ID NOS: 1276209
; SEQ ID NO 485168
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: probe
; NAME/KEY: misc feature
; LOCATION: (1)..(25)
; OTHER INFORMATION: SEQ ID NO: 14491; WAN01UQID; Start 1354; Stop 1378;
; OTHER INFORMATION: 00000000001000
US-11-348-413-485168

Query Match          59.2%; Score 14.2; DB 9; Length 25;
Best Local Similarity 47.4%; Pred. No. 3.1e+03;
Matches 9; Conservative 7; Mismatches 3; Indels 0; Gaps 0;

QY 4 UGUCUCUCUUCGCCACC 22
Db 23 TGTCTTTCCTTTAACCACC 5

RESULT 12
US-11-348-413-485634/c
; Sequence 485634, Application US/11348413
; Publication No. US20060160121A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; APPLICANT: Murphy, Ellen
; APPLICANT: Olmsted, Stephen
; TITLE OF INVENTION: PROBE ARRAYS FOR DETECTING MULTIPLE STRAINS OF DIFFERENT SPECIES
; FILE REFERENCE: 031896-084100 (AM 101724)
; CURRENT APPLICATION NUMBER: US/11/348,413
; CURRENT FILING DATE: 2006-02-07
; PRIOR APPLICATION NUMBER: PCT/US05/035471
; PRIOR FILING DATE: 2005-10-05
; PRIOR APPLICATION NUMBER: US 11/243,445
; PRIOR FILING DATE: 2005-10-05
; PRIOR APPLICATION NUMBER: US 60/615,573
; PRIOR FILING DATE: 2004-10-05
; NUMBER OF SEQ ID NOS: 1276209
; SEQ ID NO 485634
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; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: probe
; NAME/KEY: misc feature
; LOCATION: (1)..(25)
; OTHER INFORMATION: SEQ ID NO: 14505; WAN01UQIX; Start 1590; Stop 1614;
; OTHER INFORMATION: 000000000010000
US-11-348-413-485634

Query Match          59.2%; Score 14.2; DB 9; Length 25;
Best Local Similarity 47.4%; Pred. No. 3.1e+03;
Matches 9; Conservative 7; Mismatches 3; Indels 0; Gaps 0;

QY 2 AUUGUCUCUCUUCGCCCA 20
Db 25 AGTGTCTCTCTTCTCTCCA 7

RESULT 13
US-11-348-413-485635/c
; Sequence 485635, Application US/11348413
; Publication No. US20060160121A1
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; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; APPLICANT: Murphy, Ellen
; APPLICANT: Olmsted, Stephen
; TITLE OF INVENTION: PROBE ARRAYS FOR DETECTING MULTIPLE STRAINS OF DIFFERENT SPECIES
; FILE REFERENCE: 031896-084100 (AM 101724)
; CURRENT APPLICATION NUMBER: US/11/348,413
; CURRENT FILING DATE: 2006-02-07
; PRIOR FILING DATE: 2005-10-05
; PRIOR APPLICATION NUMBER: PCT/US05/035471
; PRIOR FILING DATE: 2005-10-05
; PRIOR APPLICATION NUMBER: US 11/243,445
; PRIOR FILING DATE: 2005-10-05
; PRIOR APPLICATION NUMBER: US 60/615,573
; PRIOR FILING DATE: 2004-10-05
; NUMBER OF SEQ ID NOS: 1276209
; SEQ ID NO 485635
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: probe
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(25)
; OTHER INFORMATION: SEQ ID NO: 14505; WAN01UQIX; Start 1592; Stop 1616;
; OTHER INFORMATION: 00000000010000
US-11-348-413-485635

Query Match          59.2%; Score 14.2; DB 9; Length 25;
Best Local Similarity 47.4%; Pred. No. 3.1e+03;
Matches 9; Conservative 7; Mismatches 3; Indels 0; Gaps 0;

QY      2 AUGUGUCUCUCUUGGCCA 20
Db      23 AGTGTCTCTCTTCTCCCA 5
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; Publication No. US20060160121A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; APPLICANT: Murphy, Ellen
; APPLICANT: Olmsted, Stephen
; TITLE OF INVENTION: PROBE ARRAYS FOR DETECTING MULTIPLE STRAINS OF DIFFERENT SPECIES
; FILE REFERENCE: 031896-084100 (AM 101724)
; CURRENT APPLICATION NUMBER: PCT/US05/035471
; CURRENT FILING DATE: 2006-02-07
; PRIOR FILING DATE: 2005-10-05
; PRIOR APPLICATION NUMBER: US 11/243,445
; PRIOR FILING DATE: 2005-10-05
; PRIOR APPLICATION NUMBER: US 60/615,573
; PRIOR FILING DATE: 2004-10-05
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; NAME/KEY: misc feature
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; OTHER INFORMATION: 111111100000000
US-11-348-413-689385

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Best Local Similarity 36.8%; Pred. No. 3.1e+03;
Matches 9; Conservative 7; Mismatches 3; Indels 0; Gaps 0;

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Matches 7; Conservative 9; Mismatches 3; Indels 0; Gaps 0;

QY      1 UAUGUGUCUCUCUUGGCC 19
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; Publication No. US20060160121A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; APPLICANT: Murphy, Ellen
; APPLICANT: Olmsted, Stephen
; TITLE OF INVENTION: PROBE ARRAYS FOR DETECTING MULTIPLE STRAINS OF DIFFERENT SPECIES
; FILE REFERENCE: 031896-084100 (AM 101724)
; CURRENT APPLICATION NUMBER: US/11/348,413
; CURRENT FILING DATE: 2006-02-07
; PRIOR FILING DATE: 2005-10-05
; PRIOR APPLICATION NUMBER: PCT/US05/035471
; PRIOR FILING DATE: 2005-10-05
; PRIOR APPLICATION NUMBER: US 11/243,445
; PRIOR FILING DATE: 2005-10-05
; PRIOR APPLICATION NUMBER: US 60/615,573
; PRIOR FILING DATE: 2004-10-05
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; SEQ ID NO 861056
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: probe
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(25)
; OTHER INFORMATION: SEQ ID NO: 7205; WAN01UM2G_at; Start 114; Stop 138;
; OTHER INFORMATION: 000000001100000
US-11-348-413-861056

Query Match          59.2%; Score 14.2; DB 9; Length 25;
Best Local Similarity 47.4%; Pred. No. 3.1e+03;
Matches 9; Conservative 7; Mismatches 3; Indels 0; Gaps 0;

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Db      24 ATAGTCTCTTCTTAGCCA 6
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Search completed: October 16, 2006, 14:22:02
Job time : 53.2331 secs

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	5	15.8	18.6	25	2	AX447886	Sequence
	6	15.4	18.1	28	2	AR770823	Sequence
	7	15.4	18.1	28	2	AX234378	Sequence
	8	15.4	18.1	30	2	AR004751	Sequence
	9	15.4	18.1	30	2	AR008237	Sequence
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	12	15.4	18.1	30	2	177021	Sequence 81
	13	15.4	18.1	30	2	I81016	Sequence 81
14	15.4	18.1	30	2	I81112	Sequence 81	
15	15.2	17.9	21	2	CS226910	Sequence	
16	15.2	17.9	21	2	CS226911	Sequence	
17	15.2	17.9	20	2	CS188766	Sequence	
18	15	17.6	17	2	AX215298	Sequence	

KEYWORDS JP 2002517245-A/8.
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE other sequences; artificial sequences.
AUTHORS 1 (bases 1 to 30)
Linnik,M.D.
TITLE Therapeutic and diagnostic domain 1-beta-2GPI polypeptide and method of using the same
JOURNAL Patent: JP 2002517245-A 8 18-JUN-2002;
LA JOLLA PHARMACEUTICAL CO
COMMENT OS Artificial Sequence
PN JP 2002517245-A/8
PD 18-JUN-2002
PF 09-JUN-1999 JP 2000553585
PR 09-JUN-1998 US 60/088656,05-OCT-1998 US 60/103088 PR
08-JUN-1999 US 09/328199
PI DAVID M MARQUIS,GILBERT M IVERSON,EDWARD J VICTORIA,DAVID S JONES,
PI MATTHEW D LINNIK
PC C12N15/09,A61K38/00,A61K39/385,A61K47/48,A61P37/02,C07K14/47,
PC C07K14/775,
PC C07K19/00,C12N1/15,C12N1/19,C12N1/21,C12N5/10,G01N33/69,C12N15/00,
CC A61K37/02,C12N5/00
CC synthetic construct
FH Key Location/Qualifiers
FT source 1..30
FT /organism="Artificial Sequence".
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Best Local Similarity 58.6%; Pred. No. 1.3e+06;
Matches 17; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
QY 25 UGUUAAGGCGUCCCAAGUUGAAGGC 53
Db 2 TGGTGATGGTGGCCACAACTTGGCATGGC 30
RESULT 3
LOCUS AR639871 30 bp DNA linear PAT 20-APR-2005
DEFINITION Sequence 18 from patent US 6858210.
ACCESSION AR639871
VERSION AR639871.1 GI:62773956
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 30)
AUTHORS Marquis,D.M., Iverson,G.M., Victoria,E.J., Jones,D.S. and Linnik,M.D.
TITLE Therapeutic and diagnostic domain 1 .beta.2GPI polypeptides and methods of using same
JOURNAL Patent: US 6858210-A 18 22-FEB-2005;
La Jolla Pharmaceutical Co.; San Diego, CA
FEATURES Location/Qualifiers
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/mol_type="genomic DNA"
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Best Local Similarity 58.6%; Pred. No. 1.3e+06;
Matches 17; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

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Db 2 TGGTGATGGTGGCCACAACTTGGCATGGC 30
RESULT 4
LOCUS AX443910 24 bp DNA linear PAT 03-JUL-2002
DEFINITION Sequence 365 from Patent WO0216649.
ACCESSION AX443910
VERSION AX443910.1 GI:21691188
KEYWORDS synthetic construct
ORGANISM synthetic construct
REFERENCE 1 other sequences; artificial sequences.
AUTHORS Gunderson,K.
TITLE Probes and decoder oligonucleotides
JOURNAL Patent: WO 0216649-A 365 28-FEB-2002;
Illumina, Inc. (US)
FEATURES Location/Qualifiers
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/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Computer Generated Probe Sequence."
ORIGIN
Query Match 18.6%; Score 15.8; DB 2; Length 24;
Best Local Similarity 73.7%; Pred. No. 1.8e+06;
Matches 14; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
QY 16 GAGAGGCGUGGUUAAGGC 34
Db 4 GAGAGGCGTTGGTTAAGGC 22
RESULT 5
LOCUS AX447886 25 bp DNA linear PAT 03-JUL-2002
DEFINITION Sequence 4341 from Patent WO0216649.
ACCESSION AX447886
VERSION AX447886.1 GI:21696785
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1 Gunderson,K.
AUTHORS Probes and decoder oligonucleotides
TITLE Patent: WO 0216649-A 4341 28-FEB-2002;
JOURNAL Illumina, Inc. (US)
FEATURES Location/Qualifiers
source 1..25
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Computer Generated Probe Sequence."
ORIGIN
Query Match 18.6%; Score 15.8; DB 2; Length 25;
Best Local Similarity 73.7%; Pred. No. 1.8e+06;
Matches 14; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
QY 16 GAGAGGCGUGGUUAAGGC 34
Db 5 GAGAGGCGTTGGTTAAGGC 23
RESULT 6
LOCUS AR770823 28 bp DNA linear PAT 08-DEC-2005
DEFINITION Sequence 28 from patent US 6965010.

[illegible]

REFERENCE
1 (bases 1 to 30)
AUTHORS
Skolnick, M.H.; Goldgar, D.E.; Miki, Y.; Swenson, J.; Kamb, A.

Best Local Similarity 36.0%; Pred. No. 2.6e+06;
Matches 9; Conservative 10; Mismatches 6; Indels 0; Gaps 0;

QY 55 CUUUGCUUCUGUUUUCUGGAUCAG 79
|: :||: :||: :||: :||
Db 6 CTCGTGTTGTTCTCTCTCTCCAG 30

RESULT 11
BD105661
LOCUS 30 bp DNA linear PAT 27-AUG-2002
DEFINITION Genes sensitive to 17q-chained breast cancer and ovarian cancer.
ACCESSION BD105661
VERSION BD105661.1 GI:22651235
KEYWORDS JP 2001346593-A/79.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Homo.
1 (bases 1 to 30)
Skolnick,M.H., Goldgar,D.E., Miki,Y., Swenson,J., Kamb,A.,
Harshman,K.D., Eidens,D.M.S., Tavtigian,S.V., Wiseman,R.W. and
Futreal,A.P.
Genes sensitive to 17q-chained breast cancer and ovarian cancer
Patent: JP 2001346593-A 79 18-DEC-2001;
MYRIAD GENETICS INC,UNIVERSITY OF UTAH RESEARCH FOUNDATION, THE
UNITED STATES OF AMERICA
OS Homo sapiens (human)
PN JP 2001346593-A/79
PD 18-DEC-2001
PF 18-APR-2001 JP 2001119644
PR 12-AUG-1994 US 08/289221,02-SEP-1994 US 08/300266 PR
16-SEP-1994 US 08/308104,29-NOV-1994 US 08/348824 PR
24-MAR-1995 US 08/409305,07-JUN-1995 US 08/483554 PR
07-JUN-1995 US 08/487002
PI MARK H SKOLNICK,DAVID E GOLDFAR,YOSHIO MIKI,JEFF SWENSON, PI
ALEXANDER KAMB
PI KEITH D HARSHMAN,DONNA M SHATTUCK EIDENS,SEAN V TAVTIGIAN, PI
ROGER W WISEMAN,
ANDREW P FUTREAL
PC C12N15/09,C12N1/15,C12N1/19,C12N1/21,C12N5/10,C12Q1/68,C12N15/
PC 00.C12N5/00
CC Strandedness: Single;
CC Topology: Linear;
CC Genes sensitive to 17q-chained breast cancer and ovarian CC
cancer

PH Key Location/Qualifiers
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/organism='Homo sapiens (human)'.
FEATURES
source 1..30
Location/Qualifiers
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/mol_type="genomic DNA"
/db_xref="taxon:9606"

ORIGIN
Query Match 18.1%; Score 15.4; DB 2; Length 30;
Best Local Similarity 36.0%; Pred. No. 2.6e+06;
Matches 9; Conservative 10; Mismatches 6; Indels 0; Gaps 0;

QY 55 CUUUGCUUCUGUUUUCUGGAUCAG 79
|: :||: :||: :||: :||
Db 6 CTCGTGTTGTTCTCTCTCTCCAG 30

RESULT 12
I77021
LOCUS 30 bp DNA linear PAT 03-APR-1998
DEFINITION Sequence 81 from patent US 5693473.
ACCESSION I77021
VERSION I77021.1 GI:3013175
KEYWORDS

SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 30)
AUTHORS Shattuck-Eidens,D.M., Simard,J., Durocher,F., Emi,M. and Nakamura,Y.
TITLE Linked breast and ovarian cancer susceptibility gene
JOURNAL Patent: US 5693473-A 81 02-DEC-1997;
FEATURES Location/Qualifiers
source 1..30
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN
Query Match 18.1%; Score 15.4; DB 2; Length 30;
Best Local Similarity 36.0%; Pred. No. 2.6e+06;
Matches 9; Conservative 10; Mismatches 6; Indels 0; Gaps 0;

QY 55 CUUUGCUUCUGUUUUCUGGAUCAG 79
|: :||: :||: :||: :||
Db 6 CTCGTGTTGTTCTCTCTCTCCAG 30

RESULT 13
I81016
LOCUS 30 bp DNA linear PAT 10-JUN-1998
DEFINITION Sequence 81 from patent US 5709999.
ACCESSION I81016
VERSION I81016.1 GI:3209306
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 30)
AUTHORS Shattuck-Eidens,D.M., Simard,J., Durocher,F., Emi,M. and Nakamura,Y.
TITLE Linked breast and ovarian cancer susceptibility gene
JOURNAL Patent: US 5709999-A 81 20-JAN-1998;
FEATURES Location/Qualifiers
source 1..30
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN
Query Match 18.1%; Score 15.4; DB 2; Length 30;
Best Local Similarity 36.0%; Pred. No. 2.6e+06;
Matches 9; Conservative 10; Mismatches 6; Indels 0; Gaps 0;

QY 55 CUUUGCUUCUGUUUUCUGGAUCAG 79
|: :||: :||: :||: :||
Db 6 CTCGTGTTGTTCTCTCTCTCCAG 30

RESULT 14
I81112
LOCUS 30 bp DNA linear PAT 10-JUN-1998
DEFINITION Sequence 81 from patent US 5710001.
ACCESSION I81112
VERSION I81112.1 GI:3209402
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 30)
AUTHORS Skolnick,M.H., Goldgar,D.E., Miki,Y., Swenson,J., Kamb,A., Harshman,K.D., Shattuck-Eidens,D.M., Tavtigian,S.V., Wiseman,R.W. and Futreal,P.Andrew.
TITLE 17q-linked breast and ovarian cancer susceptibility gene
JOURNAL Patent: US 5710001-A 81 20-JAN-1998;
FEATURES Location/Qualifiers
source 1..30
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN

Query Match 18.1%; Score 15.4; DB 2; Length 30;
Best Local Similarity 36.0%; Pred. No. 2.6e+06;
Matches 9; Conservative 10; Mismatches 6; Indels 0; Gaps 0;

QY 55 CUUUGCUUCUGUUUUCUGGAGCAG 79
|: :||: :||: :||: :||
Db 6 CTCGTGTGTCTCTCTCTCTCCAG 30

RESULT 15

CS226910
LOCUS CS226910 21 bp DNA linear PAT 15-DEC-2005
DEFINITION Sequence 12 from Patent WO2005103713.

ACCESSION CS226910
VERSION CS226910.1 GI:83691771

KEYWORDS

SOURCE Homo sapiens (human)

ORGANISM

Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.

REFERENCE

1.

AUTHORS Merchiers, P.G.

TITLE Methods, compositions and compound assays for inhibiting

amyloid-beta protein production

JOURNAL Patent: WO 2005103713-A 12 03-NOV-2005;

Galapagos Genomics N.V. (BE)

FEATURES

source Location/Qualifiers

1..21

/organism="Homo sapiens"

/mol_type="unassigned DNA"

/db_xref="taxon:9606"

ORIGIN

Query Match 17.9%; Score 15.2; DB 2; Length 21;
Best Local Similarity 40.0%; Pred. No. 3.1e+06;
Matches 8; Conservative 9; Mismatches 3; Indels 0; Gaps 0;

QY 53 CGCUUUGCUUCUGUUUUCUG 72
|: :||: :||: :||: :||

Db 1 CACTTGTCTCTCTCTCTCTG 20

Search completed: October 16, 2006, 14:52:14

Job time : 2094.41 secs

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RESULT 2
US-09-328-199-18
; Sequence 18, Application US/09328199
; Patent No. 6858210
; GENERAL INFORMATION:
; APPLICANT: Marquis, M. David
; APPLICANT: Iverson, M. Gilbert
; APPLICANT: Victoria, J. Edward
; APPLICANT: Jones, S. David
; APPLICANT: Linnik, Matthew
; TITLE OF INVENTION: THERAPEUTIC AND DIAGNOSTIC DOMAIN 1
; TITLE OF INVENTION: (2GP) POLYPEPTIDES AND METHODS OF USING SAME
; FILE REFERENCE: 252312006900
; CURRENT APPLICATION NUMBER: US/09/328,199

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; CURRENT FILING DATE: 1999-06-09
; EARLIER APPLICATION NUMBER: 60/088,656
; EARLIER FILING DATE: 1998-06-09
; EARLIER APPLICATION NUMBER: 60/103,088
; EARLIER FILING DATE: 1998-10-05
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 18
; LENGTH: 30
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic construct
US-09-328-199-18

Query Match      19.1%; Score 16.2; DB 3; Length 30;
Best Local Similarity 58.6%; Pred. No. 9.7e+03;
Matches 17; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

QY 25 UGUUAGGCGUCCCAAGUUGGAGGCG 53
Db 2 TGGTGATGGTGGCCACCAACTTGGCATGC 30

RESULT 3
US-09-396-196G-2452/C
; Sequence 2452, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2452
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-396-196G-2452

Query Match      18.8%; Score 16; DB 3; Length 25;
Best Local Similarity 41.7%; Pred. No. 1.1e+04;
Matches 10; Conservative 9; Mismatches 5; Indels 0; Gaps 0;

QY 61 UUCUGUUUUCUGAUGCAGAGUCC 84
Db 24 TTGCTTCTCTGGATCAAGAGTCC 1

RESULT 4
US-09-396-196G-119516
; Sequence 119516, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 119516
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-396-196G-119516

Query Match      18.8%; Score 16; DB 3; Length 25;
Best Local Similarity 45.8%; Pred. No. 1.1e+04;
Matches 11; Conservative 8; Mismatches 5; Indels 0; Gaps 0;

QY 61 UUCUGUUUUCUGAUGCAGAGUCC 84
Db 1 TCGTGTTCCTGGCTACAAAGTCC 24

RESULT 5
US-09-396-196G-119517
; Sequence 119517, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 119517
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-396-196G-119517

Query Match      18.8%; Score 16; DB 3; Length 25;
Best Local Similarity 45.8%; Pred. No. 1.1e+04;
Matches 11; Conservative 8; Mismatches 5; Indels 0; Gaps 0;

QY 61 UUCUGUUUUCUGAUGCAGAGUCC 84
Db 2 TCGTGTTCCTGGCTACAAAGTCC 25

RESULT 6
US-09-396-196G-119518
; Sequence 119518, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 119518
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-396-196G-119518

Query Match      18.4%; Score 15.6; DB 3; Length 25;
Best Local Similarity 50.0%; Pred. No. 1.5e+04;
Matches 11; Conservative 7; Mismatches 4; Indels 0; Gaps 0;
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QY 63 CUGUUUUCUGGAGUCGAGUCC 84
Db 1 CTGTTTGTGCTACAAAGTCC 22

RESULT 7
US-09-396-196G-10620
; Sequence 10620, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 10620
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-396-196G-10620

Query Match 18.1%; Score 15.4; DB 3; Length 25;
Best Local Similarity 68.0%; Pred. No. 1.8e+04;
Matches 17; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 30 AAGCGUCCCAAGUUGAAGGCG 54
Db 1 AAGCATCCCCAACGTGCTAGCGC 25

RESULT 8
US-09-396-196G-10621
; Sequence 10621, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 10621
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-396-196G-10621

Query Match 18.1%; Score 15.4; DB 3; Length 25;
Best Local Similarity 68.0%; Pred. No. 1.8e+04;
Matches 17; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 31 AGCGUCCCAAGUUGAAGGCGC 55
Db 1 AGGCATCCCCAACGTGCTAGCGC 25

RESULT 9
US-09-396-196G-20972
; Sequence 20972, Application US/09396196G
; Patent No. 6965010
; GENERAL INFORMATION:
; APPLICANT: Alitalo et al
; TITLE OF INVENTION: MATERIALS AND METHODS INVOLVING HYBRID VASCULAR
; FILE REFERENCE: 28967/35977B
; CURRENT APPLICATION NUMBER: US/09/795,006A
; CURRENT FILING DATE: 2001-02-26
; PRIOR APPLICATION NUMBER: US 60/205,331
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; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 20972
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-396-196G-20972

Query Match 18.1%; Score 15.4; DB 3; Length 25;
Best Local Similarity 60.0%; Pred. No. 1.8e+04;
Matches 15; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 40 CAAUUGAAGGCGCCUUGCUUCU 64
Db 1 CAACTGGAAGGCGCGAGGCTTAT 25

RESULT 10
US-09-396-196G-50927/c
; Sequence 50927, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 50927
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-396-196G-50927

Query Match 18.1%; Score 15.4; DB 3; Length 25;
Best Local Similarity 44.0%; Pred. No. 1.8e+04;
Matches 11; Conservative 8; Mismatches 6; Indels 0; Gaps 0;

QY 60 CUUCUGUUUUGGAGUCCAGUCC 84
Db 25 CTTGTGTCATCTGTGTGAAGTCC 1

RESULT 11
US-09-795-006A-28
; Sequence 28, Application US/09795006A
; Patent No. 6965010
; GENERAL INFORMATION:
; APPLICANT: Alitalo et al
; TITLE OF INVENTION: MATERIALS AND METHODS INVOLVING HYBRID VASCULAR
; FILE REFERENCE: 28967/35977B
; CURRENT APPLICATION NUMBER: US/09/795,006A
; CURRENT FILING DATE: 2001-02-26
; PRIOR APPLICATION NUMBER: US 60/205,331
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; PRIOR FILING DATE: 2000-05-18
; PRIOR APPLICATION NUMBER: US 60/185,205
; PRIOR FILING DATE: 2000-02-25
; NUMBER OF SEQ ID NOS: 175
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 28
; LENGTH: 28
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Artificial chimeric
; OTHER INFORMATION: oligonucleotide sequence derived from multiple vertebrate vascula
; OTHER INFORMATION: endothelial growth factor
US-09-795-006A-28

Query Match          18.1%; Score 15.4; DB 4; Length 28;
Best Local Similarity 64.0%; Pred. No. 1.9e+04;
Matches 16; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 2 GGUUUCUGCAACUGAGAGGGGCGUG 26
Db 3 GGGTCTGCAATAGTGAGGGGCTG 27

RESULT 12
US-08-480-784-81
; Sequence 81, Application US/08480784
; Patent No. 5693473
; GENERAL INFORMATION:
; APPLICANT: Skolnick, Mark H.
; APPLICANT: Goldgar, David E.
; APPLICANT: Miki, Yoshio
; APPLICANT: Swenson, Jeff
; APPLICANT: Kamb, Alexander
; APPLICANT: Harshman, Keith D.
; APPLICANT: Shattuck-Eidens, Donna M.
; APPLICANT: Tavtigian, Sean V.
; APPLICANT: Wiseman, Roger W.
; APPLICANT: Futreal, P. Andrew
; TITLE OF INVENTION: 17q-Linked Breast and Ovarian Cancer
; NUMBER OF SEQUENCES: 85
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP
; STREET: 1201 New York Avenue, N.W., Suite 1000
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/480,784
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/409,305
; FILING DATE: 24-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/348,824
; FILING DATE: 29-NOV-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/308,104
; FILING DATE: 16-SEP-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/308,104
; FILING DATE: 02-SEP-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/289,221
; FILING DATE: 12-AUG-1994
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```
; ATTORNEY/AGENT INFORMATION:
; NAME: Ihnen, Jeffrey L.
; REGISTRATION NUMBER: 28,957
; REFERENCE/DOCKET NUMBER: 24884-109347
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-962-4810
; TELEFAX: 202-962-8300
; INFORMATION FOR SEQ ID NO: 81:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 30 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; US-08-480-784-81

Query Match          18.1%; Score 15.4; DB 2; Length 30;
Best Local Similarity 36.0%; Pred. No. 2e+04;
Matches 9; Conservative 10; Mismatches 6; Indels 0; Gaps 0;

QY 55 CUUGCUUCUGUUUCUGGAGUCAG 79
Db 6 CTCCTGTTGTCTCTCTCTCCAG 30

RESULT 13
US-08-483-553-81
; Sequence 81, Application US/08483553
; Patent No. 5709999
; GENERAL INFORMATION:
; APPLICANT: Skolnick, Mark H.
; APPLICANT: Goldgar, David E.
; APPLICANT: Miki, Yoshio
; APPLICANT: Swenson, Jeff
; APPLICANT: Kamb, Alexander
; APPLICANT: Harshman, Keith D.
; APPLICANT: Shattuck-Eidens, Donna M.
; APPLICANT: Tavtigian, Sean V.
; APPLICANT: Wiseman, Roger W.
; APPLICANT: Futreal, P. Andrew
; TITLE OF INVENTION: 17q-Linked Breast and Ovarian Cancer
; NUMBER OF SEQUENCES: 85
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP
; STREET: 1201 New York Avenue, N.W., Suite 1000
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/483,553
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/409,305
; FILING DATE: 24-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/348,824
; FILING DATE: 29-NOV-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/308,104
; FILING DATE: 16-SEP-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/300,266
; FILING DATE: 12-AUG-1994
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; FILING DATE: 02-SEP-1994
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/289,221
 ; FILING DATE: 12-AUG-1994
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Ihnen, Jeffrey L.
 ; REGISTRATION NUMBER: 28,957
 ; REFERENCE/DOCKET NUMBER: 24884-109347
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 202-962-4810
 ; TELEFAX: 202-962-8300
 ; INFORMATION FOR SEQ ID NO: 81:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 30 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: DNA (genomic)
 ; HYPOTHETICAL: NO
 ; ORIGINAL SOURCE:
 ; ORGANISM: Homo sapiens
 ; US-08-483-553-81

Query Match 18.1%; Score 15.4; DB 2; Length 30;
 Best Local Similarity 36.0%; Pred. No. 2e+04;
 Matches 9; Conservative 10; Mismatches 6; Indels 0; Gaps 0;

QY 55 CUUUGCUUCUUGUUUCUGAUGCAG 79
 | : ||| : : ||| : : |||
 Db 6 CTCGCTTGTTCTCTGTCCTCCAG 30

RESULT 14
 US-08-487-002-81
 ; Sequence 81, Application US/08487002
 ; Patent No. 5710001
 ; GENERAL INFORMATION:
 ; APPLICANT: Shattuck-Eidens, Donna M.
 ; APPLICANT: Simard, Jacques
 ; APPLICANT: Emi, Mitsu
 ; APPLICANT: Nakamura, Yusuke
 ; APPLICANT: Durocher, Francine
 ; TITLE OF INVENTION: 17q-Linked Breast and Ovarian Cancer
 ; NUMBER OF SEQUENCES: 85
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP
 ; STREET: 1201 New York Avenue, N.W., Suite 1000
 ; CITY: Washington
 ; STATE: DC
 ; COUNTRY: USA
 ; ZIP: 20005
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/487,002
 ; FILING DATE:
 ; CLASSIFICATION: 424
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/409,305
 ; FILING DATE: 24-MAR-1995
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/348,824
 ; FILING DATE: 29-NOV-1994
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/308,104
 ; FILING DATE: 16-SEP-1994
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/300,266
 ; FILING DATE: 02-SEP-1994

; FILING DATE: 02-SEP-1994
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/289,221
 ; FILING DATE: 12-AUG-1994
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Ihnen, Jeffrey L.
 ; REGISTRATION NUMBER: 28,957
 ; REFERENCE/DOCKET NUMBER: 24884-109347
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 202-962-4810
 ; TELEFAX: 202-962-8300
 ; INFORMATION FOR SEQ ID NO: 81:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 30 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: DNA (genomic)
 ; HYPOTHETICAL: NO
 ; ORIGINAL SOURCE:
 ; ORGANISM: Homo sapiens
 ; US-08-483-553-81

Query Match 18.1%; Score 15.4; DB 2; Length 30;
 Best Local Similarity 36.0%; Pred. No. 2e+04;
 Matches 9; Conservative 10; Mismatches 6; Indels 0; Gaps 0;

QY 55 CUUUGCUUCUUGUUUCUGAUGCAG 79
 | : ||| : : ||| : : |||
 Db 6 CTCGCTTGTTCTCTGTCCTCCAG 30

RESULT 15
 US-08-483-554B-81
 ; Sequence 81, Application US/08483554B
 ; Patent No. 5747282
 ; GENERAL INFORMATION:
 ; APPLICANT: Skolnick, Mark H.
 ; APPLICANT: Goldgar, David E.
 ; APPLICANT: Miki, Yoshio
 ; APPLICANT: Swenson, Jeff
 ; APPLICANT: Kamb, Alexander
 ; APPLICANT: Harshman, Keith D.
 ; APPLICANT: Shattuck-Eidens, Donna M.
 ; APPLICANT: Tavtigian, Sean V.
 ; APPLICANT: Wiseman, Roger W.
 ; APPLICANT: Futreal, P. Andrew
 ; TITLE OF INVENTION: 17q-Linked Breast and Ovarian Cancer
 ; NUMBER OF SEQUENCES: 85
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP
 ; STREET: 1201 New York Avenue, N.W., Suite 1000
 ; CITY: Washington
 ; STATE: DC
 ; COUNTRY: USA
 ; ZIP: 20005
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/483,554B
 ; FILING DATE: 07-JUN-1995
 ; CLASSIFICATION: 514
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/409,305
 ; FILING DATE: 24-MAR-1995
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/348,824
 ; FILING DATE: 29-NOV-1994
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/308,104

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; FILING DATE: 16-SEP-1994
; PRIOR APPLICATION DATA: US 08/300,266
; FILING DATE: 02-SEP-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/289,221
; FILING DATE: 12-AUG-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Ihnen, Jeffrey L.
; REGISTRATION NUMBER: 28,957
; REFERENCE/DOCKET NUMBER: 24884-109347
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-962-4810
; TELEFAX: 202-962-8300
; INFORMATION FOR SEQ ID NO: 81:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 30 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
;
US-08-483-554B-81
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Query Match      18.1%; Score 15.4; DB 2; Length 30;
Best Local Similarity 36.0%; Pred. No. 2e+04;
Matches 9; Conservative 10; Mismatches 6; Indels 0; Gaps 0;

Qy      55 CUUUGCUUCUGUUUUGUGGAGCAG 79
      |:|:|:|:|:|:|:|:|:|:|:|:|:|
Db      6 CTCGTGTTGTGTTCTCTGTCTCCAG 30
```

Search completed: October 16, 2006, 14:47:13
Job time : 197.842 secs

GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 16, 2006, 14:04:23 ; Search time 3655.64 Seconds
(without alignments)
1300.222 Million cell updates/sec

Title: US-10-604-726A-6033
Perfect score: 85
Sequence: 1 ggguaucugcaacugagag.....uuuucuggaagcagaguccu 85

Scoring table: IDENTITY NUC
Gapop 10_0 , Gapext 1.0

Searched: 48236798 seqs, 27959665780 residues

Total number of hits satisfying chosen parameters: 56556

Minimum DB seq length: 0
Maximum DB seq length: 30

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

EST:*

1: gb_est1:*
2: gb_est3:*
3: gb_est4:*
4: gb_est5:*
5: gb_est6:*
6: gb_est7:*
7: gb_est8:*
8: gb_est9:*
9: gb_est10:*
10: gb_est11:*
11: gb_est12:*
12: gb_est13:*
13: gb_est14:*
14: gb_est15:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	16.2	19.1	25	13	CZ910028
C 2	16	18.8	30	10	H25855 y153h05.s1
C 3	15.4	18.1	22	11	AZ814281
4	15.4	18.1	28	11	AZ583022
C 5	14.6	17.2	25	9	D19580 MUSGS00987
6	14.4	16.9	29	11	BZ292979 SALK_1290
7	14.2	16.7	20	11	AZ469472 1M0283A06
8	14.2	16.7	23	11	AZ785027 2M0028H03
9	14	16.5	24	11	AZ806300 2M0068F13
10	13.4	15.8	26	2	BF732161 EST-NGR-1
C 11	13.4	15.8	27	11	AZ763057 1M0558C22
C 12	13.4	15.8	27	14	AJ591134 Arabidops
C 13	13.4	15.8	29	11	BH792654 SALK_0648
C 14	13.4	15.8	29	11	BH809983 SALK_0368
C 15	13.2	15.5	27	9	DN955347 it86c09.g
C 16	13.2	15.5	28	1	AA961904 or68c12.s
C 17	13.2	15.5	28	13	CZ482297 e04545-5p
18	13.2	15.5	28	14	AJ531105 Arabidops
19	13.2	15.5	29	13	CZ471342 d00034-5p

C 20	13	15.3	28	11	BH851575
C 21	13	15.3	30	11	AZ788334 2M0035B19
C 22	12.8	15.1	21	14	AJ527468 Arabidops
23	12.8	15.1	25	1	AI143800
24	12.8	15.1	27	11	AZ320101 1M0040B04
25	12.8	15.1	27	14	AG203779 Pan trogl
C 26	12.8	15.1	28	13	CZ469769
C 27	12.8	15.1	28	13	CZ471273 C07136-3p
C 28	12.8	15.1	30	11	AZ375590 1M0129H06
C 29	12.6	14.8	27	11	AZ876196 2M0191A12
30	12.6	14.8	28	11	AZ832180 2M0112J24
C 31	12.6	14.8	28	11	BH790976 SALK_0583
32	12.6	14.8	28	13	CZ481452 e03694-5p
33	12.6	14.8	29	11	AZ309550 1M0016A11
34	12.6	14.8	30	13	CZ194878
35	12.6	14.8	30	13	CZ488898 f06234-5p
36	12.4	14.6	22	14	TA219C09P
C 37	12.4	14.6	24	11	BZ356062 SALK_1280
38	12.4	14.6	25	11	AZ945526 2M0206L22
39	12.4	14.6	26	14	AG190196 Pan trogl
40	12.4	14.6	26	14	TA216H03P
41	12.4	14.6	27	5	CF311022
42	12.4	14.6	28	8	CX011229 i051b09.b
43	12.4	14.6	28	10	DV227849 EST-AR161
44	12.4	14.6	28	11	AZ802448 2M0061B20
45	12.4	14.6	28	14	AJ598500 Arabidops

ALIGNMENTS

RESULT 1
CZ910028/c
LOCUS
DEFINITION 4018012H11.LEL.y1 4018 - RescueMu Grid X Zea mays genomic, genomic survey sequence.
ACCESSION CZ910028
VERSION CZ910028.1 GI:71923396
KEYWORDS GSS.
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.
REFERENCE 1 (bases 1 to 25)
AUTHORS Walbot V.
TITLE Maize genomic sequences found using engineered RescueMu transposon
JOURNAL Unpublished (2001)
COMMENT Contact: Walbot V
Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
Email: walbot@stanford.edu
Very probable ligation site of ends cut by single endonuclease.
Reverse complemented post-ligation sequence from source sequence.
Plate: 4018012 row: H column: 11
Class: transposon-tagged.

FEATURES

source
1..25
/organism="Zea mays"
/mol_type="genomic DNA"
/cultivar="mixed background W23/A188/B73/K55"
/db_xref="taxon:4577"
/tissue_type="leaf"
/lab_host="DH10B"
/clone_lib="4018 - RescueMu Grid X"
/note="Organ: leaf; Vector: RescueMu (engineered from pBlueScript backbone); Site 1: BamHI; Site 2: BglII; RescueMu is a 4.9 kb, modified maize Mu transposon designed to allow plasmid rescue from total genomic DNA."

Mu elements insert preferentially into transcription units. For more information on RescueMu, go to the web site <http://www.mutransposon.org/project/RescueMu/>. Grid X was grown at UCSD in 2003. DNA was extracted from leaf strips, double digested using BamHI and BglII, and ligated to form circular plasmids. DH10B cells were transformed and then screened on LB plates with ampicillin."

```

ORIGIN
Query Match      19.1%; Score 16.2; DB 13; Length 25;
Best Local Similarity 38.1%; Pred. No. 1.3e+06;
Matches 8; Conservative 10; Mismatches 3; Indels 0; Gaps 0;

QY 50 GGCGCGUUGCUUCUGUUC 70
Db 23 GGCGCTCTTTGTTTGTTC 3

RESULT 2
H25855/C
LOCUS
DEFINITION
H25855 30 bp mRNA linear EST 10-JUL-1995
Y153n05.s1 Soares breast 3NBH8ct Homo sapiens cDNA clone
IMAGE:162009 3' similar to gb:S71043_rnal IG ALPHA-2 CHAIN C REGION
(HUMAN);, mRNA sequence.

ACCESSION
H25855
VERSION
H25855.1 GI:894978
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominoidea; Homo.
REFERENCE
1 (bases 1 to 30)
Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
Trevasakis,E., Waterston,R., Williamson,A., Wohldmann,P. and
Wilson,R.
The WashU-Merck EST Project
Unpublished (1995)
Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@wustl.wustl.edu
Insert Size: 934
High quality sequence starts: 1
High quality sequence stops: 1
Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Trace considered overall poor quality
Insert Length: 934 Std Error: 0.00
Seq primer: Promega -21m13
High quality sequence stop: 1.
FEATURES
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1. .30
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="GDB:576220"
/db_xref="taxon:9606"
/clone="IMAGE:162009"
/sex="female"
/dev_stage="adult"
/lab_host="DH10B (ampicillin resistant)"
/clone_lib="Soares breast 3NBH8ct"
/notes="Organ: breast; Vector: pT7T3D (Pharmacia) with a
modified Polylinker; site 1: Not I; Site 2: Eco RI; 1st
strand cDNA was primed with a Not I - oligo(dT) primer [5',
TGTACCAATCTGAAGTGGAGCGCCGCTTTTGTTC 3'],
double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not I

```

and Eco RI sites of a modified pT7T3 vector (Pharmacia). Library went through one round of normalization to a Cot = 20. Library constructed by Bento Soares and M.Fatima Bonaldo."

```

ORIGIN
Query Match      18.8%; Score 16; DB 10; Length 30;
Best Local Similarity 66.7%; Pred. No. 1.5e+06;
Matches 16; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 37 CCCCAAGUUGGAAGCGCUUUGC 60
Db 29 CCTCAAGTGGGAAGAGCGCTGTC 6

RESULT 3
AZ814281
LOCUS
DEFINITION
2M0082L04F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC2M0082L04 F, genomic survey sequence.

ACCESSION
AZ814281
VERSION
AZ814281.1 GI:12984285
KEYWORDS
GSS.
SOURCE
Mus musculus (house mouse)
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridea; Muridae; Murinae; Mus.
REFERENCE
1 (bases 1 to 22)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D. Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0082 row: 1 column: 04
Seq primer: CGTTGTAAACGACGCGCCAGT
Class: plasmid ends
High quality sequence stop: 22.
FEATURES
source
1. .22
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0082L04"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, TI-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated

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Insert Length: 10000 Std Error: 0.00
 Plate: 0028 row: H column: 03
 Seq primer: CACACAGGAACAGCTATGACC
 Class: plasmid ends
 High quality sequence stop: 23.
 Location/Qualifiers

FEATURES

source

1..23

/organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC2M0028H03"
 /sex="Male"

/lab_host="E. Coli strain XL10-Gold, TI-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 16.7%; Score 14.2; DB 11; Length 23;

Best Local Similarity 63.2%; Pred. No. 5.9e+06;

Matches 12; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 5 UAUCGACACAGAGAGGGG 23

|||||
 2 TGCTCAGCTGAGGGGG 20

RESULT 9

AZ806300

LOCUS

AZ806300 24 bp DNA linear GSS 20-FEB-2001
 clone UUGC2M0068F13 F, genomic survey sequence.

ACCESSION

AZ806300

VERSION

GSS.1

GI:12967111

Mus musculus (house mouse)

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;

Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 24)

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,

Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,

Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von

Niederhauser,A. and Wright,D. Weiss,R.

Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts

Unpublished (2000)

Contact: Robert B. Weiss

University of Utah Genome Center

University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0068 row: F column: 13
 Seq primer: CGTTGTAAACGACGCCAGT
 Class: plasmid ends
 High quality sequence stop: 24.
 Location/Qualifiers

FEATURES

source

1..24

/organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC2M0068F13"
 /sex="Male"

/lab_host="E. Coli strain XL10-Gold, TI-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 16.5%; Score 14; DB 11; Length 24;

Best Local Similarity 59.1%; Pred. No. 6.9e+06;

Matches 13; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 12 AACUGAGGGGCGUGGUUAGG 33

|||||
 2 AAGTGGAGTGGGTGAGG 23

RESULT 10

BF732161

LOCUS

BF732161 26 bp mRNA linear EST 30-MAY-2001
 EST-NGR-1-39 mouse GR-1+ myeloid progenitor cells cDNA Library Mus

musculus cDNA 3', mRNA sequence.

ACCESSION

BF732161

VERSION

EST.

GI:14249781

Mus musculus (house mouse)

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;

Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 26)

Chen,J., Rowley,D.A., Clark,T., Lee,S., Zhou,G., Beer,C.,

Rowley,J.D. and Wang,S.M.

Pattern of gene expression in mouse GR-1+ myeloid progenitor cells

Unpublished (2001)

Contact: Wang SM

Hem/Onc

University of Chicago Medical Center

5841 S. Maryland Ave., MC2115, Chicago, IL 60637, USA

Tel: 773-702-6788

Fax: 773-702-3002

Email: swanglomidway.uchicago.edu

This EST fragment was amplified from mouse GR-1+ myeloid progenitor

cells cDNA Library with GLGI technique (Generation of Longer cDNA

/note="T-DNA flanking sequence
left border"

ORIGIN
Query Match 15.8%; Score 13.4; DB 14; Length 27;
Best Local Similarity 73.3%; Pred. No. 1.1e+07;
Matches 11; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 19 AGGGGCGGUUAAGG 33

Db 21 AGGGGCTGGTTACG 7

RESULT 13
BH792654/c
LOCUS
DEFINITION
SALK_064849 48.70 x Arabidopsis thaliana TDNA insertion lines
Arabidopsis thaliana genomic clone SALK_064849.48.70.x, genomic
survey sequence.

ACCESSION
BH792654

VERSION
BH792654.1 GI:19889664

SOURCE
Arabidopsis thaliana (thale cress)

ORGANISM
Arabidopsis thaliana

REFERENCE
1 (bases 1 to 29)
Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R.,
Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L.,
Shinn,P., Zimmerman,J. and Ecker,J.R.
A Sequence-Indexed Library of Insertion Mutations in the
Arabidopsis Genome

AUTHORS
Unpublished (2001)

TITLE
Contact: Joseph R. Ecker

JOURNAL
Salk Institute Genomic Analysis Laboratory (SIGAL)

COMMENT
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
Email: ecker@salk.edu
This is single pass sequence recovered from the left border of
TDNA.

Class: TDNA tagged.

Location/Qualifiers

1. 29

/organism="Arabidopsis thaliana"

/mol_type="genomic DNA"

/ecotype="Col-0"

/db_xref="taxon:3702"

/clone_lib="Arabidopsis thaliana TDNA insertion lines"

/note="PCR was performed on Arabidopsis thaliana lines

each of which contains one or more TDNA insertion

elements. The resultant fragment for each line was

directly sequenced to determine the genomic sequence at

the site of insertion. Details of the protocols used can

be found at http://signal.salk.edu/tdna_protocols.html

ORIGIN

Query Match 15.8%; Score 13.4; DB 11; Length 29;

Best Local Similarity 43.5%; Pred. No. 1.1e+07;

Matches 10; Conservative 7; Mismatches 6; Indels 0; Gaps 0;

QY 44 UUGGAGGCGGUUUGCUUCUGU 66

Db 23 TTGGAGCGGTGCTATGCTGT 1

RESULT 14

BH809983/c

LOCUS

DEFINITION

SALK_036896 Arabidopsis thaliana TDNA insertion lines Arabidopsis

survey sequence.

ACCESSION

VERSION

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Contact: W. Richard McCombie

Lita Annenberg Hazen Genome Sequencing Center

Cold Spring Harbor Laboratory

PO Box 100, Cold Spring Harbor, NY 11724, USA

ACCESSION
BH809983

VERSION
BH809983.1 GI:20387800

SOURCE
Arabidopsis thaliana (thale cress)

ORGANISM
Arabidopsis thaliana

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Contact: Joseph R. Ecker

Salk Institute Genomic Analysis Laboratory (SIGAL)

The Salk Institute for Biological Studies

10010 N. Torrey Pines Road, La Jolla, CA 92037, USA

Tel: 858 453 4100 x1752

Fax: 858 558 6379

Email: ecker@salk.edu

This is single pass sequence recovered from the left border of

TDNA.

Class: TDNA tagged.

Location/Qualifiers

1. 29

/organism="Arabidopsis thaliana"

/mol_type="genomic DNA"

/ecotype="Col-0"

/db_xref="taxon:3702"

/clone_lib="Arabidopsis thaliana TDNA insertion lines"

/note="PCR was performed on Arabidopsis thaliana lines

each of which contains one or more TDNA insertion

elements. The resultant fragment for each line was

directly sequenced to determine the genomic sequence at

the site of insertion. Details of the protocols used can

be found at http://signal.salk.edu/tdna_protocols.html

ORIGIN

Query Match 15.8%; Score 13.4; DB 11; Length 29;

Best Local Similarity 43.5%; Pred. No. 1.1e+07;

Matches 10; Conservative 7; Mismatches 6; Indels 0; Gaps 0;

QY 44 UUGGAGGCGGUUUGCUUCUGU 66

Db 23 TTGGAGCGGTGCTATGCTGT 1

RESULT 15

LOCUS

DEFINITION

SALK_036896 Arabidopsis thaliana TDNA insertion lines Arabidopsis

survey sequence.

ACCESSION

VERSION

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Contact: W. Richard McCombie

Lita Annenberg Hazen Genome Sequencing Center

Cold Spring Harbor Laboratory

PO Box 100, Cold Spring Harbor, NY 11724, USA

thaliana genomic clone SALK_036896, genomic survey sequence.

ACCESSION

VERSION

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Contact: Joseph R. Ecker

Salk Institute Genomic Analysis Laboratory (SIGAL)

The Salk Institute for Biological Studies

10010 N. Torrey Pines Road, La Jolla, CA 92037, USA

Tel: 858 453 4100 x1752

Fax: 858 558 6379

Email: ecker@salk.edu

This is single pass sequence recovered from the left border of

TDNA.

Class: TDNA tagged.

Location/Qualifiers

1. 29

/organism="Arabidopsis thaliana"

/mol_type="genomic DNA"

/ecotype="Col-0"

/db_xref="taxon:3702"

/clone_lib="Arabidopsis thaliana TDNA insertion lines"

/note="PCR was performed on Arabidopsis thaliana lines

each of which contains one or more TDNA insertion

elements. The resultant fragment for each line was

directly sequenced to determine the genomic sequence at

the site of insertion. Details of the protocols used can

be found at http://signal.salk.edu/tdna_protocols.html

ORIGIN

Query Match 15.8%; Score 13.4; DB 11; Length 29;

Best Local Similarity 43.5%; Pred. No. 1.1e+07;

Matches 10; Conservative 7; Mismatches 6; Indels 0; Gaps 0;

QY 44 UUGGAGGCGGUUUGCUUCUGU 66

Db 23 TTGGAGCGGTGCTATGCTGT 1

RESULT 15

LOCUS

DEFINITION

SALK_036896 Arabidopsis thaliana TDNA insertion lines Arabidopsis

survey sequence.

ACCESSION

VERSION

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Contact: W. Richard McCombie

Lita Annenberg Hazen Genome Sequencing Center

Cold Spring Harbor Laboratory

PO Box 100, Cold Spring Harbor, NY 11724, USA

Tel: 516 367 8884
Fax: 516 367 8874
Email: mcombie@cshl.org
Seq primer: -21Mi3UnivRev.

FEATURES

source
1. .27
Location/Qualifiers
/organism="Gnetum gnemon"
/mol_type="mRNA"
/db_xref="taxon:3382"
/sex="female"
/clone_lib="Gnetum female cone (NYBG)"
/notes="Organ: mature, unfertilized reproductive strobili;
Vector: pBK-CMV; Site 1: XhoI; Site 2: Eco RI; Date:
Completed 02/11/02, submitted for sequencing 02/12/02.
Library: Stratagene ZAP Express cDNA Synthesis kit. The
library was size-fractionated to enrich for large inserts.
Sample: NYBG accession number #436/84"

ORIGIN

Query Match 15.5%; Score 13.2; DB 9; Length 27;
Best Local Similarity 50.0%; Pred. No. 1.3e+07;
Matches 9; Conservative 6; Mismatches 3; Indels 0; Gaps 0;
Qy 50 GGGCGCUCUCUCUCUCU 67
||||| :|:|:|:|:|:
Db 27 GGGCGTTTGTCTGCT 10

Search completed: October 16, 2006, 15:51:26
Job time : 3658.64 secs

GenCore version 5.1.1.9
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 16, 2006, 13:53:09 ; Search time 444.812 Seconds
(without alignments)
1332.341 Million cell updates/sec

Title: US-10-604-726A-6033

Perfect score: 85

Sequence: 1 ggguaucugcaacagagag.....uuuucggaugcagaguccu 85

Scoring table: IDENTITY NUC

Gapop 10_0 , Gapext 1.0

Searched: 5244920 seqs, 3486124231 residues

Total number of hits satisfying chosen parameters: 4443654

Minimum DB seq length: 0

Maximum DB seq length: 30

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_8.*

- 1: Geneseqn1980s.*
- 2: Geneseqn1990s.*
- 3: Geneseqn2000s.*
- 4: Geneseqn2001as.*
- 5: Geneseqn2001bs.*
- 6: Geneseqn2002as.*
- 7: Geneseqn2002bs.*
- 8: Geneseqn2003as.*
- 9: Geneseqn2003bs.*
- 10: Geneseqn2003cs.*
- 11: Geneseqn2003ds.*
- 12: Geneseqn2004as.*
- 13: Geneseqn2004bs.*
- 14: Geneseqn2005s.*
- 15: Geneseqn2006s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	17.2	20.2	26	6 AAD25159	Aad25159 Human NOV
C 2	17.2	20.2	26	11 ADK51090	Adk51090 Human NOV
C 3	16.2	19.1	23	10 ADE03643	Ade03643 BGS PCR p
C 4	16.2	19.1	29	4 AAH74161	Aah74161 Human neu
C 5	16.2	19.1	30	3 AAZ29694	Aaz29694 Oligonucl
6	16.2	19.1	30	14 AED56453	Aed56453 Human ost
7	15.8	18.6	24	6 ABQ11002	Abq11002 Oligonucl
8	15.8	18.6	24	6 ABQ04674	Abq04674 Oligonucl
C 9	15.8	18.6	24	6 ABQ04715	Abq04715 Oligonucl
C 10	15.8	18.6	24	6 ABQ00358	Abq00358 Oligonucl
C 11	15.8	18.6	24	6 ABQ11043	Abq11043 Oligonucl
C 12	15.8	18.6	25	6 ABQ12538	Abq12538 Oligonucl
C 13	15.8	18.6	25	6 ABQ12579	Abq12579 Oligonucl
14	15.6	18.4	30	14 ADY01452	Ady01452 PCR prime
15	15.6	18.4	30	14 ADY03184	Ady03184 PCR prime
16	15.6	18.4	30	14 ADX84276	Adx84276 DNA ampli
17	15.6	18.4	30	14 AED57194	Aed57194 Human ost
18	15.6	18.4	30	14 AED57246	Aed57246 Human ost

c	19	15.6	18.4	30	15	AEF08297	Asf08297 LOC115209
	20	15.4	18.1	25	9	ACI82438	ACI82438 Human mic
	21	15.4	18.1	28	4	AA512826	AA512826 Human VEG
	22	15.4	18.1	30	14	ADK84134	Adk84134 DNA ampli
	23	15.2	17.9	20	12	ADK75812	Adk75812 Chimeric
	24	15.2	17.9	21	12	ADQ61714	Adq61714 Anti-NR1D
	25	15.2	17.9	21	14	ABE01688	Abe01688 G protein
	26	15.2	17.9	21	14	ABE01687	Abe01687 G protein
c	27	15.2	17.9	25	9	ACK26430	Ack26430 Human mic
	28	15.2	17.9	28	2	AAT74315	Aat74315 PCR prime
	29	15.2	17.9	29	15	ABE67632	Abe67632 Human Hun
	30	15.2	17.9	30	12	ADO05844	Ado05844 Teneurin-
	31	15.2	17.9	30	12	ADX99810	Adx99810 PCR prime
c	32	15	17.6	17	4	ABK00741	Abk00741 Human NOG
	33	15	17.6	17	4	ABK00742	Abk00742 Human NOG
	34	15	17.6	17	4	ABK00740	Abk00740 Human NOG
	35	15	17.6	23	14	AEC92288	Aec92288 Human IRT
	36	15	17.6	24	2	AAH78730	Aah78730 Dengue vi
c	37	15	17.6	24	2	ABA94895	Abas94895 Dengue vi
	38	15	17.6	24	14	AEA40055	Aea40055 Brassica
	39	15	17.6	25	1	AAH80648	Aan80648 Sequence
	40	15	17.6	25	1	AAH80647	Aan80647 Sequence
	41	15	17.6	25	9	ACI58550	ACI58550 Human mic
	42	15	17.6	25	9	ACI59178	ACI59178 Human mic
	43	15	17.6	26	2	AAQ72851	Aaq72851 Primer 32
	44	14.8	17.4	20	10	ABZ89358	Abz89358 Human oli
c	45	14.8	17.4	20	11	ABD25588	Abd25588 AI001174-

ALIGNMENTS

RESULT 1

AAD25159/c

ID AAD25159 standard; DNA; 26 BP.

XX AAD25159;

AC AAD25159;

DT 12-MAR-2002 (first entry)

XX Human NOV4 gene expression assessing Ag1252 probe.

DE Human; NOV4; gene therapy; atherosclerosis; cardiomyopathy; leukaemia;
KW neurological; neurodegenerative disease; cell signalling; inflammation;
KW diabetes; seizure; muscular dystrophy; epilepsy; allergy; adenocarcinoma;
KW coagulation disorder; reproductive; respiratory; bone; nephrological;
KW multiple sclerosis; mental depression; gastro-intestinal disease; cancer;
KW urinary system disorder; Addison's disease; migraine; dermatomyositis;
KW bronchitis; probe; ss.

XX Homo sapiens.

XX Key Location/Qualifiers

FT modified_base 1 /tag= a

FT /mod_base= OTHER

FT /note= "FAM labelled adenosine"

FT modified_base 26

FT /tag= b

FT /mod_base= OTHER

FT /note= "TAMRA labelled thymidine"

XX WO200194416-A2.

XX 13-DEC-2001.

XX 07-JUN-2001; 2001WO-US018675.

XX 07-JUN-2000; 2000US-0209927P.

XX 07-JUN-2000; 2000US-0209928P.

XX 07-JUN-2000; 2000US-0210091P.

XX 08-JUN-2000; 2000US-0210208P.

XX 08-JUN-2000; 2000US-0210425P.

XX US2003195163-A1.
XX 16-OCT-2003.
XX 11-JUL-2002; 2002US-00193477.
XX 11-JUL-2001; 2001US-0304888P.
XX 12-APR-2002; 2002US-0372147P.
XX (WUSS/) WU S.
XX (KEYS/) KRISTEK S R.
XX (LEBL/) LEE L.
XX (FEDE/) FEDER J N.
XX (CHEN/) CHENG J D.
XX Wu S, Krystek SR, Lee L, Feder JN, Cheng JD;
XX WPI; 2003-844480/78.
XX
XX New isolated nucleic acid molecule encoding BGS-2, 3 and 4 polypeptides,
XX useful for preventing, treating or ameliorating a medical condition, e.g.
XX a disorder related to aberrant immunoglobulin cell surface receptor
XX activity.
XX
XX Example 4; SEQ ID NO 228; 242bp; English.
XX
XX The invention relates to an isolated nucleic acid molecule encoding BGS-
XX 2, 3 and 4 polypeptides. The nucleic acid molecule, polypeptide and
XX methods are useful for preventing, treating or ameliorating a medical
XX condition, such as a disorder related to aberrant immunoglobulin cell
XX surface receptor activity; a cellular adhesion disorder; a disorder
XX related to hyper- or hypo-immunoglobulin receptor activity; a disorder
XX related to aberrant signal transduction; a reproductive disorder; a
XX female reproductive disorder; an ovarian disorder; ovarian cancer, sexual
XX dysfunction; infertility; pelvic inflammatory disease; endometriosis;
XX premature menopause; placental dysfunction; hormone deficiency; oestrogen
XX deficiency; aberrant androgen metabolism; polycystic ovarian disease;
XX aberrant ovarian cycle; dysfunctional uterine bleeding; resistant-ovary
XX syndrome; hermaphroditism; immune disorders; inflammatory disorders;
XX arthritis; asthma; immunodeficiency diseases such as AIDS; leukaemia;
XX inflammatory bowel disease; sepsis; acne; psoriasis; hypersensitivity;
XX such as T-cell mediated cytotoxicity; immune reactions to transplanted
XX organs and tissues; or autoimmune disorders; autoimmune infertility;
XX Addison's disease; haemolytic anaemia; rheumatoid arthritis; dermatitis;
XX glomerulonephritis; Graves' Disease; Multiple Sclerosis; Myasthenia
XX Gravis; Systemic Lupus Erythematosus; insulin dependent diabetes mellitus
XX ; autoimmune inflammatory eye disease; Sjogren's disease; and
XX scleroderma. The present sequence is used in the exemplification of the
XX present invention.
XX
XX Sequence 23 BP; 2 A; 4 C; 5 G; 12 T; 0 U; 0 Other;
XX
XX Query Match 19.1%; Score 16.2; DB 10; Length 23;
XX Best Local Similarity 38.1%; Pred. No. 4.1e+04;
XX Matches 8; Conservative 10; Mismatches 3; Indels 0; Gaps 0;
XX
XX QY 52 GCGCUUGUCUUGUUUUUCUG 72
XX ||||| : : : : :
XX 1 GCGCTTTGATTATGTTCTCTG 21
XX
XX RESULT 4
XX AAH74161/c
XX ID AAH74161 standard; DNA; 29 BP.
XX AC AAH74161;
XX
XX 09-OCT-2001 (first entry)
XX
XX Human neuronal calcium sensor protein 1 related oligonucleotide #6.
XX
XX Human neuronal calcium sensor protein 1; NCS-1; primer; ds.
XX

XX Unidentified.
XX CN1287171-A.
XX 14-MAR-2001.
XX 07-SEP-1999; 99CN-00118819.
XX 07-SEP-1999; 99CN-00118819.
XX (UYFU-) UNIV FUDAN.
XX Yu L, Fu Q, Zhao Y;
XX WPI; 2001-398934/43.
XX Human neuron calcium sensing protein and its code sequence, preparation
XX and use.
XX
XX Example 4; Page 13(Disclosure); 21pp; Chinese.
XX
XX The present invention provides the cDNA sequence of human neuronal
XX calcium sensor protein 1 (NCS-1). The NCS-1 protein is a member of the
XX neuronal calcium ion binding protein family and a homologue of human NCS-
XX 1. The present invention also relates to the protein, the application of
XX the polynucleotide and the polypeptide, and the production process of the
XX polynucleotide and the polypeptide
XX
XX Sequence 29 BP; 6 A; 8 C; 7 G; 8 T; 0 U; 0 Other;
XX
XX Query Match 19.1%; Score 16.2; DB 4; Length 29;
XX Best Local Similarity 58.6%; Pred. No. 4.4e+04;
XX Matches 17; Conservative 4; Mismatches 8; Indels 0; Gaps 0;
XX
XX QY 14 CUGAGAGGGGUGUUAAGGCGUCCCA 42
XX | : ||||| : : : : :
XX 29 CTACGACGGCTGCTATAGGAATTCCTCA 1
XX
XX RESULT 5
XX AAZ29694
XX ID AAZ29694 standard; DNA; 30 BP.
XX AC AAZ29694;
XX 22-MAR-2000 (first entry)
XX
XX Oligonucleotide B2del242-326 for domain deletion mutant of hbeta-2 GPI.
XX
XX Human beta-2 glycoprotein I; hbeta-2 GPI; beta-2 GPI domain 1;
XX oligonucleotide B2del242-326; sushi domain;
XX beta-2 GPI-dependent antiphospholipid antibody; ss.
XX
XX Homo sapiens.
XX Synthetic.
XX
XX WO9964595-A1.
XX
XX 16-DEC-1999.
XX
XX 09-JUN-1999; 99WO-US013194.
XX
XX 09-JUN-1998; 98US-0088656P.
XX 05-OCT-1998; 98US-0103088P.
XX 08-JUN-1999; 99US-00328199.
XX
XX (LJOL-) LA JOLLA PHARM CO.
XX
XX Marquis DM, Iverson GM, Victoria EJ, Jones DS, Linnik MD;
XX WPI; 2000-116542/10.
XX

PT New isolated domain 1 beta-2 GPI polypeptides, used for inhibiting
PT antiphospholipid antibodies for treating, e.g. thrombosis.
XX
PS
PS Example 1; Page 51; 158pp; English.
XX
CC The present sequence is oligonucleotide B2del242-326 used for generating
CC domain deletion mutant of human beta-2 glycoprotein I. Isolated domain I
CC of beta-2 GPI binds to and inhibits beta-2 GPI-dependent antiphospholipid
CC antibodies. Amino acids 242-326 are deleted from beta-2 GPI and the
CC resulting protein contains 1, 2, 3 and 4 sushi domains. This is used to
CC determine the antigenic regions of beta-2 GPI
XX
XX Sequence 30 BP; 6 A; 6 C; 11 G; 7 T; 0 U; 0 Other;
XX
Query Match 19.1%; Score 16.2; DB 3; Length 30;
Best Local Similarity 58.6%; Pred. No. 4.5e+04;
Matches 17; Conservative 4; Mismatches 8; Indels 0; Gaps 0;
XX
QY 25 UGUUUAAGGCGUCCCAAGUGGAGGGC 53
Db 2 TGTGTGTTGGCCCACTTGCATGGC 30
XX
RESULT 6
AED56453
ID AED56453 standard; DNA; 30 BP.
XX
AC AED56453;
XX
DT 29-DEC-2005 (first entry)
XX
DE Human osteoporosis related SNP primer #413.
XX
XX osteoarthritis; musculoskeletal disease; Antiarthritic; Osteopathic;
KW RNAi; RNAi interference; ADAMTS2 agonist; ss; PCR; primer.
XX
XX Homo sapiens.
XX
FN WO2005100604-A2.
XX
PD 27-OCT-2005.
XX
XX 31-MAR-2005; 2005WO-US010912.
XX
PR 01-APR-2004; 2004US-0559011P.
PR 01-APR-2004; 2004US-0559040P.
PR 01-APR-2004; 2004US-0559042P.
PR 01-APR-2004; 2004US-0559202P.
PR 01-APR-2004; 2004US-0559203P.
PR 01-APR-2004; 2004US-0559225P.
PR 01-APR-2004; 2004US-0559275P.
XX
PA (SEQU-) SEQUENOM INC.
XX
XX Mah S, Braun A, Kammerer SM, Nelson MR, Reneland RH, Langdown ML;
XX
XX WPI; 2005-758634/77.
XX
XX Identifying a subject at risk of osteoarthritis comprises detecting the
PT presence or absence of one or more specified polymorphic variations
PT associated with osteoarthritis in a nucleic acid sample from a subject.
XX
XX Example 5; Page 88; 539pp; English.
PS
XX The invention relates to a method of identifying a subject at risk of
CC osteoarthritis which comprises detecting the presence or absence of one
CC or more polymorphic variations associated with osteoarthritis in a
CC nucleic acid sample where the presence of the polymorphism indicates a
CC risk of osteoarthritis. The method is useful for identifying a subject at
CC risk of osteoarthritis. The method is also useful for identifying agents
CC for treating osteoarthritis. The present sequence represents a PCR primer
CC used to identify single nucleotide polymorphisms associated with
XX osteoporosis.
XX

XX
SQ Sequence 30 BP; 4 A; 3 C; 12 G; 11 T; 0 U; 0 Other;
XX
Query Match 19.1%; Score 16.2; DB 14; Length 30;
Best Local Similarity 41.4%; Pred. No. 4.5e+04;
Matches 12; Conservative 9; Mismatches 8; Indels 0; Gaps 0;
XX
QY 41 AAGUUGGAAGGCGCUUUGCUUCUGUUU 69
Db 1 ACGTTGGATGAGTGTCTTCAGGTGTGT 29
XX
RESULT 7
ABQ11002
ID ABQ11002 standard; DNA; 24 BP.
XX
AC ABQ11002;
XX
DT 11-JUN-2002 (first entry)
XX
DE Oligonucleotide adapter/capture probe 10993.
XX
KW Oligonucleotide array; adapter sequence; probe; ss.
XX
OS Synthetic.
XX
XX WO200216649-A2.
PN
PD 28-FEB-2002.
XX
XX 27-AUG-2001; 2001WO-US026519.
XX
PR 25-AUG-2000; 2000US-0227948P.
PR 29-AUG-2000; 2000US-0228854P.
XX
XX (ILLU-) ILLUMINA INC.
XX
XX Gunderson K;
XX
XX WPI; 2002-292068/33.
XX
XX Array comprising adapter sequences useful for immobilizing or detecting a
PT target nucleic acid sequence, has different addresses comprising
PT different specific capture probes.
XX
XX Claim 1; Page 225; 261pp; English.
XX
XX The invention relates to an oligonucleotide array (I) comprising at least
CC 25 different addresses (adapter sequences) with each comprising a
CC different capture probe selected from a group consisting of the sequences
CC given in ABQ00010-ABQ13409. (I) is useful for immobilising a target
CC nucleic acid sequence by attaching a adapter nucleic acid (ABQ00010-
CC ABQ13409) to a target nucleic acid to form a modified target nucleic acid
CC and contacting the modified target nucleic acid with (I). The steps of
CC above method is useful for detecting a target nucleic acid, which further
CC comprises detecting the presence of the modified target nucleic acid
XX
XX Sequence 24 BP; 7 A; 2 C; 10 G; 5 T; 0 U; 0 Other;
XX
Query Match 18.6%; Score 15.8; DB 6; Length 24;
Best Local Similarity 73.7%; Pred. No. 5.9e+04;
Matches 14; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
XX
QY 16 GAGAGGCGCGUUAAGGC 34
Db 4 GAGAGCGTTGTTAAGGC 22
XX
RESULT 8
ABQ04674
ID ABQ04674 standard; DNA; 24 BP.
XX
XX ABQ04674;
AC

XX	11-JUN-2002	(first entry)
DT		
DE	Oligonucleotide adapter/capture probe 4665.	
XX		
KW	Oligonucleotide array; adapter sequence; probe; ss.	
XX		
OS	Synthetic.	
XX		
PN	WO200216649-A2.	
XX		
PD	28-FEB-2002.	
XX		
PF	27-AUG-2001; 2001WO-US026519.	
XX		
PR	25-AUG-2000; 2000US-0227948P.	
XX		
PR	29-AUG-2000; 2000US-0228854P.	
XX		
PA	(ILLU-) ILLUMINA INC.	
XX		
PI	Gunderson K;	
XX		
DR	WPI; 2002-292068/33.	
XX		
PT	Array comprising adapter sequences useful for immobilizing or detecting a target nucleic acid sequence, has different addresses comprising different specific capture probes.	
PT		
XX		
PS	Claim 1; Page 147; 261pp; English.	
XX		
CC	The invention relates to an oligonucleotide array (I) comprising at least 25 different addresses (adapter sequences) with each comprising a different capture probe selected from a group consisting of the sequences given in ABQ00010-ABQ13409. (I) is useful for immobilising a target nucleic acid sequence by attaching a adapter nucleic acid (ABQ00010-ABQ13409) to a target nucleic acid to form a modified target nucleic acid and contacting the modified target nucleic acid with (I). The steps of above method is useful for detecting a target nucleic acid, which further comprises detecting the presence of the modified target nucleic acid	
XX		
SQ	Sequence 24 BP; 7 A; 2 C; 10 G; 5 T; 0 U; 0 Other;	
PT	Array comprising adapter sequences useful for immobilizing or detecting a target nucleic acid sequence, has different addresses comprising different specific capture probes.	
PT		
XX		
PS	Claim 1; Page 147; 261pp; English.	
XX		
CC	The invention relates to an oligonucleotide array (I) comprising at least 25 different addresses (adapter sequences) with each comprising a different capture probe selected from a group consisting of the sequences given in ABQ00010-ABQ13409. (I) is useful for immobilising a target nucleic acid sequence by attaching a adapter nucleic acid (ABQ00010-ABQ13409) to a target nucleic acid to form a modified target nucleic acid and contacting the modified target nucleic acid with (I). The steps of above method is useful for detecting a target nucleic acid, which further comprises detecting the presence of the modified target nucleic acid	
XX		
SQ	Sequence 24 BP; 7 A; 2 C; 10 G; 5 T; 0 U; 0 Other;	
Query Match	18.6%; Score 15.8; DB 6; Length 24;	
Best Local Similarity	73.7%; Pred. NO. 5.9e+04;	
Matches	14; Conservative 3; Mismatches 2; Indels 0; Gaps 0;	
QY	16 GAGAGGGCGGCUAAGGC 34 :::	
DB	4 GAGAGGGCGTGTGAAGC 22 :::	
RESULT 9		
ABQ04715/c		
ID	ABQ04715 standard; DNA; 24 BP.	
XX		
AC	ABQ04715;	
XX		
DT	11-JUN-2002 (first entry)	
XX		
DE	Oligonucleotide adapter/capture probe 4706.	
XX		
KW	Oligonucleotide array; adapter sequence; probe; ss.	
XX		
OS	Synthetic.	
XX		
PN	WO200216649-A2.	
XX		
PD	28-FEB-2002.	
XX		
PF	27-AUG-2001; 2001WO-US026519.	
XX		
PR	25-AUG-2000; 2000US-0227948P.	
XX		
PR	29-AUG-2000; 2000US-0228854P.	
XX		
PA	(ILLU-) ILLUMINA INC.	
XX		
PI	Gunderson K;	
XX		
DR	WPI; 2002-292068/33.	
XX		
PT	Array comprising adapter sequences useful for immobilizing or detecting a target nucleic acid sequence, has different addresses comprising different specific capture probes.	
PT		
XX		
PS	Claim 1; Page 147; 261pp; English.	
XX		
CC	The invention relates to an oligonucleotide array (I) comprising at least 25 different addresses (adapter sequences) with each comprising a different capture probe selected from a group consisting of the sequences given in ABQ00010-ABQ13409. (I) is useful for immobilising a target nucleic acid sequence by attaching a adapter nucleic acid (ABQ00010-ABQ13409) to a target nucleic acid to form a modified target nucleic acid and contacting the modified target nucleic acid with (I). The steps of above method is useful for detecting a target nucleic acid, which further comprises detecting the presence of the modified target nucleic acid	
XX		
SQ	Sequence 24 BP; 7 A; 2 C; 10 G; 5 T; 0 U; 0 Other;	
Query Match	18.6%; Score 15.8; DB 6; Length 24;	
Best Local Similarity	73.7%; Pred. NO. 5.9e+04;	
Matches	14; Conservative 3; Mismatches 2; Indels 0; Gaps 0;	
QY	16 GAGAGGGCGGCUAAGGC 34 :::	
DB	4 GAGAGGGCGTGTGAAGC 22 :::	
RESULT 9		
ABQ04715/c		
ID	ABQ04715 standard; DNA; 24 BP.	
XX		
AC	ABQ04715;	
XX		
DT	11-JUN-2002 (first entry)	
XX		
DE	Oligonucleotide adapter/capture probe 4706.	
XX		
KW	Oligonucleotide array; adapter sequence; probe; ss.	
XX		
OS	Synthetic.	
XX		
PN	WO200216649-A2.	
XX		
PD	28-FEB-2002.	
XX		
PF	27-AUG-2001; 2001WO-US026519.	
XX		
PR	25-AUG-2000; 2000US-0227948P.	
XX		
PR	29-AUG-2000; 2000US-0228854P.	
XX		
PA	(ILLU-) ILLUMINA INC.	
XX		
PI	Gunderson K;	
XX		
DR	WPI; 2002-292068/33.	
XX		
PT	Array comprising adapter sequences useful for immobilizing or detecting a target nucleic acid sequence, has different addresses comprising different specific capture probes.	
PT		
XX		
PS	Claim 1; Page 52; 261pp; English.	
XX		
CC	The invention relates to an oligonucleotide array (I) comprising at least 25 different addresses (adapter sequences) with each comprising a different capture probe selected from a group consisting of the sequences given in ABQ00010-ABQ13409. (I) is useful for immobilising a target nucleic acid sequence by attaching a adapter nucleic acid (ABQ00010-ABQ13409) to a target nucleic acid to form a modified target nucleic acid and contacting the modified target nucleic acid with (I). The steps of above method is useful for detecting a target nucleic acid, which further comprises detecting the presence of the modified target nucleic acid	
XX		
SQ	Sequence 24 BP; 5 A; 10 C; 2 G; 7 T; 0 U; 0 Other;	
Query Match	18.6%; Score 15.8; DB 6; Length 24;	
Best Local Similarity	73.7%; Pred. NO. 5.9e+04;	
Matches	14; Conservative 3; Mismatches 2; Indels 0; Gaps	

CC nucleic acid sequence by attaching a adapter nucleic acid (ABQ00010-
CC ABQ13409) to a target nucleic acid to form a modified target nucleic acid
CC and contacting the modified target nucleic acid with (I). The steps of
CC above method is useful for detecting a target nucleic acid, which further
CC comprises detecting the presence of the modified target nucleic acid
XX
SQ Sequence 24 BP; 7 A; 2 C; 10 G; 5 T; 0 U; 0 Other;

Query Match 18.6%; Score 15.8; DB 6; Length 24;
Best Local Similarity 73.7%; Pred. No. 5.9e+04;
Matches 14; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 16 GAGAGGGCGUGGUUAGGC 34
||||| | : : : : :
Db 4 GAGAGCGCTGGTTAAGC 22

RESULT 11
ABQ11043/c
ID ABQ11043 standard; DNA; 24 BP.
XX
AC ABQ11043;
XX
DT 11-JUN-2002 (first entry)
XX
DE Oligonucleotide adapter/capture probe 11034.
XX
KW Oligonucleotide array; adapter sequence; probe; ss.
XX
OS Synthetic.
XX
PN WO200216649-A2.
XX
PD 28-FEB-2002.

XX The invention relates to an oligonucleotide array (I) comprising at least
XX 25 different addresses (adapter sequences) with each comprising a
XX different capture probe selected from a group consisting of the sequences
XX given in ABQ00010-ABQ13409. (I) is useful for immobilising a target
XX nucleic acid sequence by attaching a adapter nucleic acid (ABQ00010-
XX ABQ13409) to a target nucleic acid to form a modified target nucleic acid
XX and contacting the modified target nucleic acid with (I). The steps of
XX above method is useful for detecting a target nucleic acid, which further
XX comprises detecting the presence of the modified target nucleic acid
XX
SQ Sequence 24 BP; 5 A; 10 C; 2 G; 7 T; 0 U; 0 Other;

Query Match 18.6%; Score 15.8; DB 6; Length 24;
Best Local Similarity 73.7%; Pred. No. 5.9e+04;
Matches 14; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 16 GAGAGGGCGUGGUUAGGC 34
||||| | : : : : :
Db 21 GAGAGCGCTGGTTAAGC 3

RESULT 12
ABQ12538
ID ABQ12538 standard; DNA; 25 BP.
XX
AC ABQ12538;
XX
DT 11-JUN-2002 (first entry)
XX
DE Oligonucleotide adapter/capture probe 12529.
XX
KW Oligonucleotide array; adapter sequence; probe; ss.
XX
OS Synthetic.
XX
PN WO200216649-A2.
XX
PD 28-FEB-2002.

XX
XX 27-AUG-2001; 2001WO-US026519.
XX
PR 25-AUG-2000; 2000US-0227948P.
PR
PR 29-AUG-2000; 2000US-0228854P.
XX
PA (ILLU-) ILLUMINA INC.
XX
PI Gunderson K;
XX
DR WPI; 2002-292068/33.
XX
PT Array comprising adapter sequences useful for immobilizing or detecting a
PT target nucleic acid sequence, has different addresses comprising
PT different specific capture probes.
XX
PS Claim 1; Page 244; 261pp; English.

XX The invention relates to an oligonucleotide array (I) comprising at least
XX 25 different addresses (adapter sequences) with each comprising a
XX different capture probe selected from a group consisting of the sequences
XX given in ABQ00010-ABQ13409. (I) is useful for immobilising a target
XX nucleic acid sequence by attaching a adapter nucleic acid (ABQ00010-
XX ABQ13409) to a target nucleic acid to form a modified target nucleic acid
XX and contacting the modified target nucleic acid with (I). The steps of
XX above method is useful for detecting a target nucleic acid, which further
XX comprises detecting the presence of the modified target nucleic acid
XX
SQ Sequence 25 BP; 7 A; 2 C; 10 G; 6 T; 0 U; 0 Other;

Query Match 18.6%; Score 15.8; DB 6; Length 25;
Best Local Similarity 73.7%; Pred. No. 6e+04;
Matches 14; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 16 GAGAGGGCGUGGUUAGGC 34
||||| | : : : : :
Db 5 GAGAGCGCTGGTTAAGC 23

RESULT 13
ABQ12579/c
ID ABQ12579 standard; DNA; 25 BP.
XX
AC ABQ12579;
XX
DT 11-JUN-2002 (first entry)
XX
DE Oligonucleotide adapter/capture probe 12570.
XX
KW Oligonucleotide array; adapter sequence; probe; ss.
XX
OS Synthetic.
XX
PN WO200216649-A2.
XX
PD 28-FEB-2002.

XX 27-AUG-2001; 2001WO-US026519.
XX 25-AUG-2000; 2000US-0227948P.
PR 29-AUG-2000; 2000US-0228854P.
XX (ILLU-) ILLUMINA INC.
PA Gunderson K;
XX WPI; 2002-292068/33.
XX Array comprising adapter sequences useful for immobilising or detecting a
PT target nucleic acid sequence, has different addresses comprising
PT different specific capture probes.
XX
XX Claim 1; Page 244; 261pp; English.
XX
XX The invention relates to an oligonucleotide array (I) comprising at least
CC 25 different addresses (adapter sequences) with each comprising a
CC different capture probe selected from a group consisting of the sequences
CC given in ABQ00010-ABQ13409. (I) is useful for immobilising a target
CC nucleic acid sequence by attaching a adapter nucleic acid (ABQ00010-
CC ABQ13409) to a target nucleic acid to form a modified target nucleic acid
CC and contacting the modified target nucleic acid with (I). The steps of
CC above method is useful for detecting a target nucleic acid, which further
CC comprises detecting the presence of the modified target nucleic acid
XX
XX Sequence 25 BP; 5 A; 10 C; 2 G; 8 T; 0 U; 0 Other;
SQ
Query Match 18.6%; Score 15.8; DB 6; Length 25;
Best Local Similarity 73.7%; Pred. No. 6e+04;
Matches 14; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
QY 16 GAGAGGGCGGUTRAGGC 34
DB 22 GAGAGCGTGTGGTTAGGC 4
RESULT 14
ADY01452
ID ADY01452 standard; DNA; 30 BP.
XX
AC ADY01452;
XX
DT 05-MAY-2005 (first entry)
XX
DE PCR primer 156 used to amplify human DPF3 SNP DNA.
XX
KW SNP detection; breast tumor; endocrine disease;
KW gynecology and obstetrics; neoplasm; cytostatic; metastasis;
KW gene therapy; RNA interference; ss; PCR; primer;
KW D4, zinc and double PHD fingers, family 3; DPF3;
KW Guanine-nucleotide exchange factor.
XX
OS Homo sapiens.
XX
PN WO2005014846-A2.
XX
PD 17-FEB-2005.
XX
PF 27-MAY-2004; 2004WO-US016939.
XX
PR 24-JUL-2003; 2003US-0490234P.
PR 25-NOV-2003; 2003US-00723681.
PR 25-NOV-2003; 2003US-0525239P.
XX
PA (SEQU-) SEQUENOM INC.
XX
PI Roth RB, Nelson MR, Braun A, Kammerer SM, Reneland R;
PI Hoyal-Wrightson CR;
XX
DR WPI; 2005-163257/17.

XX Identifying risk of, preventing and/or treating breast cancer by
PT identifying and/or analyzing polymorphic variations in nucleotide
PT sequences within the human genome.
XX
XX Example 16; Page 239; 617pp; English.
XX
XX The invention relates to a novel method for identifying a subject at risk
CC of breast cancer comprising detecting the presence or absence of a
CC polymorphic variation associated with breast cancer. The method of the
CC invention demonstrates cytostatic activity and may be useful for
CC identifying a risk of, preventing and/or treating breast cancer and
CC cancer metastasis. The methods may be utilized for gene therapy or RNA
CC interference. The current sequence is that of a PCR primer of the
CC invention which was used to amplify a human rho-family guanine-nucleotide
CC exchange factor D4, zinc and double PHD fingers, family 3 (DPF3) DNA
CC containing a single nucleotide polymorphism (SNP).
XX
XX Sequence 30 BP; 5 A; 7 C; 7 G; 11 T; 0 U; 0 Other;
SQ
Query Match 18.4%; Score 15.6; DB 14; Length 30;
Best Local Similarity 40.0%; Pred. No. 7.6e+04;
Matches 12; Conservative 9; Mismatches 9; Indels 0; Gaps 0;
QY 41 AAGUUGGAAGCGCGUUCUGUUCUUUC 70
DB 1 ACGTTGGATGGGTACATACATCTTCTGCTTC 30
RESULT 15
ADY03184
ID ADY03184 standard; DNA; 30 BP.
XX
AC ADY03184;
XX
DT 05-MAY-2005 (first entry)
XX
DE PCR primer 7 used to amplify human LOC145197 SNP DNA.
XX
KW SNP detection; breast tumor; endocrine disease;
KW gynecology and obstetrics; neoplasm; cytostatic; metastasis;
KW gene therapy; RNA interference; ds; SNP; single nucleotide polymorphism;
KW LOC145197.
XX
OS Homo sapiens.
XX
PN WO2005014846-A2.
XX
PD 17-FEB-2005.
XX
PF 27-MAY-2004; 2004WO-US016939.
XX
PR 24-JUL-2003; 2003US-0490234P.
PR 25-NOV-2003; 2003US-00723681.
PR 25-NOV-2003; 2003US-0525239P.
XX
PA (SEQU-) SEQUENOM INC.
XX
PI Roth RB, Nelson MR, Braun A, Kammerer SM, Reneland R;
PI Hoyal-Wrightson CR;
XX
DR WPI; 2005-163257/17.
XX
PT Identifying risk of, preventing and/or treating breast cancer by
PT identifying and/or analyzing polymorphic variations in nucleotide
PT sequences within the human genome.
XX
XX Example 17; Page 296; 617pp; English.
XX
XX The invention relates to a novel method for identifying a subject at risk
CC of breast cancer comprising detecting the presence or absence of a
CC polymorphic variation associated with breast cancer. The method of the
CC invention demonstrates cytostatic activity and may be useful for

CC identifying a risk of, preventing and/or treating breast cancer and
CC cancer metastasis. The methods may be utilized for gene therapy or RNA
CC interference. The current sequence is that of a PCR primer of the
CC invention which was used to amplify a human LOC145197 DNA containing a
CC single nucleotide polymorphism (SNP).
xx

SQ Sequence 30 BP; 5 A; 7 C; 8 G; 10 T; 0 U; 0 Other;

Query Match 18.4%; Score 15.6; DB 14; Length 30;
Best Local Similarity 43.3%; Pred. No. 7.6e+04;
Matches 13; Conservative 8; Mismatches 9; Indels 0; Gaps 0;

Qy 41 AAGUUGAAGGCGCUUGCUUGUUUC 70

Db 1 ACGTGGATGAGCATTTGCTCAGTTCC 30

Search completed: October 16, 2006, 14:15:59
Job time : 446.812 secs

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OM nucleic - nucleic search, using sw model

Run on: October 16, 2006, 14:16:09 ; Search time 1197.03 Seconds
(without alignments)
872.534 Million cell updates/sec

Title: US-10-604-726A-6033
Perfect score: 85
Sequence: 1 ggguaucugcaacagag.....uuucuggaugcagaguccu 85

Scoring table: IDENTITY NUC
Gapop 10_0 , Gapext 1.0

Searched: 18892170 seqs, 6143817638 residues
Total number of hits satisfying chosen parameters: 23237482

Minimum DB seq length: 0
Maximum DB seq length: 30

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications NA Main:*

- 1: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US07_PUBCOMB.seq:*
- 2: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US08_PUBCOMB.seq:*
- 3: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09A_PUBCOMB.seq:*
- 4: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
- 5: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
- 6: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
- 7: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
- 8: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10C_PUBCOMB.seq:*
- 9: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10D_PUBCOMB.seq:*
- 10: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10E_PUBCOMB.seq:*
- 11: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10F_PUBCOMB.seq:*
- 12: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10G_PUBCOMB.seq:*
- 13: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11A_PUBCOMB.seq:*
- 14: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11B_PUBCOMB.seq:*
- 15: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11C_PUBCOMB.seq:*
- 16: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11D_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	18.2	21.4	25	9	US-10-719-900-385230
2	18.2	21.4	25	9	US-10-719-900-453865
3	18.2	21.4	25	11	US-10-933-982-172709
4	18.2	21.4	26	8	US-10-403-161-111
5	18.2	21.4	27	11	US-10-310-914A-166755
6	17.8	20.9	24	10	US-10-750-185-13212
7	17.8	20.9	24	10	US-10-750-623-13212
8	17.6	20.7	24	11	US-10-310-914A-106490
9	17.6	20.7	25	13	US-11-036-317-713202
10	17.6	20.7	25	15	US-11-121-849-282693
11	17.6	20.7	25	15	US-11-121-849-386034
12	17.6	20.7	25	15	US-11-121-849-386035
13	17.6	20.7	25	15	US-11-121-849-386965
14	17.6	20.7	25	15	US-11-121-849-386966
15	17.2	20.2	24	11	US-10-310-914A-776242
16	17.2	20.2	25	9	US-10-719-900-888593
17	17.2	20.2	26	3	US-09-877-843-70

Sequence 28545, A
Sequence 411709, A
Sequence 593945, A
Sequence 15707, A
Sequence 648052, A
Sequence 705480, A
Sequence 90282, A
Sequence 989609, A
Sequence 271873, A
Sequence 568626, A
Sequence 348977, A
Sequence 614920, A
Sequence 1047378, A
Sequence 640087, A
Sequence 578380, A
Sequence 317240, A
Sequence 385229, A
Sequence 453864, A
Sequence 509279, A
Sequence 559311, A
Sequence 225474, A
Sequence 324009, A
Sequence 497082, A
Sequence 96809, A
Sequence 172712, A
Sequence 172720, A
Sequence 56788, A
Sequence 310318, A

ALIGNMENTS

RESULT 1
US-10-719-900-385230
; Sequence 385230, Application US/10719900
; Publication No. US200500261641
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 385230
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-385230

Query Match 21.4%; Score 18.2; DB 9; Length 25;
Best Local Similarity 43.5%; Pred. No. 1.4e+04;
Matches 10; Conservative 10; Mismatches 3; Indels 0; Gaps 0;
QY 58 UGUCUCUGUUUCUGAUGCAGA 80
DB 2 TCGTCTGTTTCTGAGTGATA 24
RESULT 2
US-10-719-900-453865
; Sequence 453865, Application US/10719900
; Publication No. US200500261641
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808

; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 453865
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-453865

Query Match 21.4%; Score 18.2; DB 9; Length 25;
Best Local Similarity 69.8%; Pred. No. 1.4e+04;
Matches 16; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 35 GUCCCAAGUUGAGGCGCUU 57
Db 1 GACCCCAAGTTGAAGCGGCTT 23

RESULT 3

US-10-933-982-172709/c
; Sequence 172709, Application US/10933982
; Publication No. US20060051769A1
; GENERAL INFORMATION:

; APPLICANT: Barts, Jennifer
; TITLE OF INVENTION: Methods of Genetic Analysis of E. coli
; FILE REFERENCE: 3700
; CURRENT APPLICATION NUMBER: US/10/933,982
; CURRENT FILING DATE: 2004-09-03
; NUMBER OF SEQ ID NOS: 224976
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 172709
; LENGTH: 25
; TYPE: DNA
; ORGANISM: E. coli
US-10-933-982-172709

Query Match 21.4%; Score 18.2; DB 11; Length 25;
Best Local Similarity 47.8%; Pred. No. 1.4e+04;
Matches 11; Conservative 9; Mismatches 3; Indels 0; Gaps 0;

QY 48 AAGGCGCUUUGCUUCGUUUC 70
Db 25 AAGGCGCTTACCTCTGTTTC 3

RESULT 4

US-10-403-161-111/c
; Sequence 111, Application US/10403161
; Publication No. US20040043930A1
; GENERAL INFORMATION:

; APPLICANT: Anderson, David et al.
; TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 21402-573C
; CURRENT APPLICATION NUMBER: US/10/403,161
; CURRENT FILING DATE: 2003-03-31
; PRIOR APPLICATION NUMBER: 60/370349
; PRIOR FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: 60/384543
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: 60/370969
; PRIOR FILING DATE: 2002-04-08
; PRIOR APPLICATION NUMBER: 60/403748
; PRIOR FILING DATE: 2002-08-15
; PRIOR APPLICATION NUMBER: 60/372019
; PRIOR FILING DATE: 2002-04-12
; PRIOR APPLICATION NUMBER: 60/374379
; PRIOR FILING DATE: 2002-04-22
; PRIOR APPLICATION NUMBER: 09/779679
; PRIOR FILING DATE: 2001-02-08
; PRIOR APPLICATION NUMBER: 60/181045
; PRIOR FILING DATE: 2000-02-08
; PRIOR APPLICATION NUMBER: 10/055877
; PRIOR FILING DATE: 2002-01-22

; PRIOR APPLICATION NUMBER: 60/262892
; PRIOR FILING DATE: 2001-01-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 173
; SOFTWARE: CuraSeqList version 0.1
; SEQ ID NO 111
; LENGTH: 26
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer/Probe
US-10-403-161-111

Query Match 21.4%; Score 18.2; DB 8; Length 26;
Best Local Similarity 65.2%; Pred. No. 1.4e+04;
Matches 15; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 8 CUGCAACUGAGAGGGCGUGUUA 30
Db 23 CTGCAGCTGAGAGTGTCTGGTTA 1

RESULT 5

US-10-310-914A-166755/c
; Sequence 166755, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:

; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiller, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 166755
; LENGTH: 27
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-166755

Query Match 21.4%; Score 18.2; DB 11; Length 27;
Best Local Similarity 43.5%; Pred. No. 1.4e+04;
Matches 10; Conservative 10; Mismatches 3; Indels 0; Gaps 0;

QY 50 GGGCGCUUUGCUUCGUUUUCUG 72
Db 26 GGTCCCTTTGCTTCTGTTTCTG 4

RESULT 6

US-10-750-185-13212
; Sequence 13212, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:

; APPLICANT: WMT GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-2
; CURRENT APPLICATION NUMBER: US/10/750,185
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 13212
; LENGTH: 24

```

; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Reverse Primer
US-10-750-185-13212

Query Match      20.9%; Score 17.8; DB 10; Length 24;
Best Local Similarity 38.1%; Pred. No. 2e+04;
Matches 8; Conservative 11; Mismatches 2; Indels 0; Gaps 0;

QY 56 UUUGCUUCUGUUUUCUGGAUG 76
Db 1 TTATACATCGTTTCTGGATG 21

RESULT 7
US-10-750-623-13212
; Sequence 13212, Application US/10750623
; Publication No. US20050287531A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: METHODS AND SYSTEMS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-1
; CURRENT APPLICATION NUMBER: US/10/750,623
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 13212
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Reverse Primer
US-10-750-623-13212

Query Match      20.9%; Score 17.8; DB 10; Length 24;
Best Local Similarity 38.1%; Pred. No. 2e+04;
Matches 8; Conservative 11; Mismatches 2; Indels 0; Gaps 0;

QY 56 UUUGCUUCUGUUUUCUGGAUG 76
Db 1 TTATACATCGTTTCTGGATG 21

RESULT 8
US-10-310-914A-106490/c
; Sequence 106490, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiller, Kvazut
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 106490
; LENGTH: 24
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-106490

Query Match      20.7%; Score 17.6; DB 11; Length 24;

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Result No.	Score	Query		DB	ID	Description
		Match	%			
1	17	20.0	25	9	US-11-348-413-835988	Sequence 835988, A
C 2	16.6	19.5	25	8	US-11-217-529-96809	Sequence 96809, A
3	16.4	19.3	25	8	US-11-217-529-183005	Sequence 183005, A
C 4	16.2	19.1	25	9	US-11-348-413-960036	Sequence 960036, A
5	16	18.8	25	8	US-11-217-529-52650	Sequence 52650, A
C 6	15.8	18.6	25	8	US-11-217-529-98397	Sequence 98397, A
C 7	15.6	18.4	25	8	US-11-217-529-29948	Sequence 29948, A
C 8	15.6	18.4	25	8	US-11-217-529-94477	Sequence 94477, A
9	15.6	18.4	25	8	US-11-217-529-99137	Sequence 99137, A
C 10	15.6	18.4	25	9	US-11-348-413-411718	Sequence 411718, A
C 11	15.6	18.4	25	9	US-11-348-413-414079	Sequence 414079, A
C 12	15.6	18.4	25	9	US-11-348-413-414080	Sequence 414080, A
C 13	15.6	18.4	25	9	US-11-348-413-884139	Sequence 884139, A
C 14	15.4	18.1	25	8	US-11-217-529-98618	Sequence 98618, A
C 15	15.4	18.1	25	9	US-11-348-413-350690	Sequence 350690, A
C 16	15.4	18.1	25	9	US-11-348-413-858123	Sequence 858123, A
C 17	15.4	18.1	25	9	US-11-348-413-960037	Sequence 960037, A
C 18	15.4	18.1	25	9	US-11-348-413-988357	Sequence 988357, A
C 19	15.2	17.9	25	9	US-11-348-413-411716	Sequence 411716, A
C 20	15.2	17.9	25	9	US-11-348-413-411717	Sequence 411717, A
C 21	15.2	17.9	25	9	US-11-348-413-845537	Sequence 845537, A
C 22	15.2	17.9	25	9	US-11-348-413-1052105	Sequence 1052105, A
23	15.2	17.9	30	6	US-10-530-542-17	Sequence 17, Appl

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; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 96809
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-96809

Query Match      19.5%; Score 16.6; DB 8; Length 25;
Best Local Similarity 60.9%; Pred. No. 8.9e+03;
Matches 14; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY 36 UCCCCAAGUUGGAGGCGCUU 58
Db 24 TCCCCAATTGTGAAGGCGCTT 24

RESULT 3
US-11-217-529-183005
; Sequence 183005, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 183005
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-183005

Query Match      19.3%; Score 16.4; DB 8; Length 25;
Best Local Similarity 50.0%; Pred. No. 1.1e+04;
Matches 9; Conservative 8; Mismatches 1; Indels 0; Gaps 0;

QY 62 UCUGUUUUCUGGAUGCAG 79
Db 7 TCTGTTTCTGAATGCAG 24

RESULT 4
US-11-348-413-960036/c
; Sequence 960036, Application US/11348413
; Publication No. US2006016012A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; APPLICANT: Murphy, Ellen
; APPLICANT: Olmsted, Stephen
```

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; TITLE OF INVENTION: PROBE ARRAYS FOR DETECTING MULTIPLE STRAINS OF DIFFERENT SPECIES
; FILE REFERENCE: 031896-084100 (AM 101724)
; CURRENT APPLICATION NUMBER: US/11/348,413
; CURRENT FILING DATE: 2006-02-07
; PRIOR APPLICATION NUMBER: PCT/US05/035471
; PRIOR FILING DATE: 2005-10-05
; PRIOR APPLICATION NUMBER: US 11/243,445
; PRIOR FILING DATE: 2005-10-05
; PRIOR APPLICATION NUMBER: US 60/615,573
; PRIOR FILING DATE: 2004-10-05
; NUMBER OF SEQ ID NOS: 1276209
; SEQ ID NO 960036
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: probe
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)-(25)
; OTHER INFORMATION: SEQ ID NO: 10014; WAN01PG3J_at; Start 207; Stop 231;
; OTHER INFORMATION: 00000000100000
US-11-348-413-960036

Query Match      19.1%; Score 16.2; DB 9; Length 25;
Best Local Similarity 33.3%; Pred. No. 1.3e+04;
Matches 7; Conservative 11; Mismatches 3; Indels 0; Gaps 0;

QY 55 CUUUGCUUCUGUUUCUGGAU 75
Db 23 CTTGGCTTCTGTTTCTACAT 3

RESULT 5
US-11-217-529-52650/c
; Sequence 52650, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 52650
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-52650

Query Match      18.8%; Score 16; DB 8; Length 25;
Best Local Similarity 62.5%; Pred. No. 1.5e+04;
Matches 15; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 34 CGUCCCCAAGUUGAAGGCGCUU 57
Db 24 CGTCCACGACCTGGAAGGCTCTT 1

RESULT 6
US-11-217-529-98397
; Sequence 98397, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
```

```
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; PRIOR FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 98397
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-98397

Query Match      18.6%; Score 15.8; DB 8; Length 25;
Best Local Similarity 36.8%; Pred. No. 1.1e+04;
Matches 7; Conservative 10; Mismatches 2; Indels 0; Gaps 0;

QY 54 GCUUGCUUCUGUUUCUG 72
DB 4 GCTTTGCTTCTGTTATG 22

RESULT 7
US-11-217-529-29948/c
; Sequence 29948, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 29948
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-29948

Query Match      18.4%; Score 15.6; DB 8; Length 25;
Best Local Similarity 45.5%; Pred. No. 2.1e+04;
Matches 10; Conservative 8; Mismatches 4; Indels 0; Gaps 0;

QY 64 UGUUUCUGGAGCAGAGUCCU 85
DB 24 TGTTTGGAGATGCACGCTCT 3

RESULT 8
US-11-217-529-94477/c
; Sequence 94477, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
```

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; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 94477
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-94477

Query Match      18.4%; Score 15.6; DB 8; Length 25;
Best Local Similarity 50.0%; Pred. No. 2.1e+04;
Matches 11; Conservative 7; Mismatches 4; Indels 0; Gaps 0;

QY 47 GAAGGGCGUUGCUUCUGUUU 68
DB 24 GGAGGGCGCTGTACTTCTGTCT 3

RESULT 9
US-11-217-529-99137
; Sequence 99137, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 99137
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-99137

Query Match      18.4%; Score 15.6; DB 8; Length 25;
Best Local Similarity 36.4%; Pred. No. 2.1e+04;
Matches 8; Conservative 10; Mismatches 4; Indels 0; Gaps 0;

QY 55 CUUUGCUUCUGUUUCUGAUG 76
DB 2 CTATGCTTCTATGTCTGTGTTG 23

RESULT 10
US-11-348-413-411718/c
; Sequence 411718, Application US/11348413
; Publication No. US20060160121A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; APPLICANT: Murphy, Ellen
; APPLICANT: Olmsted, Stephen
; TITLE OF INVENTION: PROBE ARRAYS FOR DETECTING MULTIPLE STRAINS OF DIFFERENT SPECIES
; FILE REFERENCE: 031896-084100 (AM 101724)
; CURRENT APPLICATION NUMBER: US/11/348,413
; CURRENT FILING DATE: 2006-02-07
; PRIOR APPLICATION NUMBER: PCT/US05/035471
; PRIOR FILING DATE: 2005-10-05
; PRIOR APPLICATION NUMBER: US 11/243,445
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, PRIOR FILING DATE: 2005-10-05
, PRIOR APPLICATION NUMBER: US 60/615,573
, PRIOR FILING DATE: 2004-10-05
, NUMBER OF SEQ ID NOS: 1276209
, SEQ ID NO 411718
, LENGTH: 25
, TYPE: DNA
, ORGANISM: Artificial
, FEATURE:
, OTHER INFORMATION: probe
, FEATURE:
, NAME/KEY: misc feature
, LOCATION: (1)..(25)
, OTHER INFORMATION: SEQ ID NO: 12488; W
US-11-348-413-411718

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Query Match      18.4%; Score 15.6; DB 9; Length 25;
Best Local Similarity 36.4%; Pred. No. 2.1e+04;
Matches 8: Conservative 10; Mismatches 4; Indels 0; Gaps 0;
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Qy 54 GCUUGCUUCUGUUUUCUGGAU 75
| : | : | : | : | : | :
Dp 25 GGGTGGTCTGTAATCTGGAT 4

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RESULT 11
US-11-348-413-414079/c
; Sequence 414079, Application US/11348413
; Publication No. US20060160121A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; APPLICANT: Murphy, Ellen
; APPLICANT: Olmsted, Stephen
; TITLE OF INVENTION: PROBE ARRAYS FOR DETECTING MULTIPLE STRAINS OF DIFFERENT SPECIES
; FILE REFERENCE: 031896-084100 (AM 101724)
; CURRENT APPLICATION NUMBER: US/11/348.413
; PRIOR FILING DATE: 2006-02-07
; PRIOR APPLICATION NUMBER: PCT/US05/035471
; PRIOR FILING DATE: 2005-10-05
; PRIOR APPLICATION NUMBER: US 11/243,445
; PRIOR FILING DATE: 2005-10-05
; PRIOR APPLICATION NUMBER: US 60/615,573
; PRIOR FILING DATE: 2004-10-05
; NUMBER OF SEQ ID NOS: 1276209
; SEQ ID NO 414079
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: probe
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(25)
; OTHER INFORMATION: SEQ ID NO: 12552; WAN01U002; Start 494; Stop 518;
; OTHER INFORMATION: 00000000011111
US-11-348-413-414079

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Query Match	18.4%	Score 15.6;	DB 9;	Length 25;
Best Local Similarity	36.4%;	Pred. No. 2.1e+04;		
Matches	8;	Conservative 10;	Mismatches 4;	Indels 0;
Gaps	0;			

QY 54 GCUUUGCUCUCUGUUUUUCUGGAU 75
||::| :: |::|::|:
Dd 25 GCATTGATTTAGTGTGCTCGAAT 4

RESULT 12
US-11-348-413-414080/c
; Sequence 414080, Application US/11348413
; Publication No. US20060160121A1
; GENERAL INFORMATION:

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1  APPLICANT: Wyeth
2  APPLICANT: Mounts, William M
3  APPLICANT: Murphy, Ellen
4  APPLICANT: Olmsted, Stephen
5  TITLE OF INVENTION: PROBE ARRAYS FOR DETECTING MULTIPLE STRAINS OF D
6  FILE REFERENCE: 031896-084100 (AM 101724)
7  CURRENT APPLICATION NUMBER: US/11/348,413
8  CURRENT FILING DATE: 2006-02-07
9  PRIOR APPLICATION NUMBER: PCT/US05/035471
10 PRIOR FILING DATE: 2005-10-05
11 PRIOR APPLICATION NUMBER: US 11/243,445
12 PRIOR FILING DATE: 2005-10-05
13 PRIOR APPLICATION NUMBER: US 60/615,573
14 PRIOR FILING DATE: 2004-10-05
15 NUMBER OF SEQ ID NOS: 1276209
16 SEQ ID NO 414080
17 LENGTH: 25
18 TYPE: DNA
19 ORGANISM: Artificial
20 FEATURE:
21 OTHER INFORMATION: probe
22 FEATURE:
23 NAME/KEY: misc feature
24 LOCATION: (1)..(25)
25 OTHER INFORMATION: SEQ ID NO: 42552; WANO1U002; Start 495; Scop 519;
26 OTHER INFORMATION: 00000000011111
27 US-11-348-413-414080

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Query Match	18.4%	Score 15.6;	DB 9;	Length 25;
Best Local Similarity	36.4%	Pred. No. 2.1e+04;		
Matches	8:	Conservative	10:	Mismatches 4;
				Indels 0;
				Gaps 0;

Qy 54 GCUUUGCUUCUGUUUUUCUGGAU 75
||::| :: |::|::|:
Db 24 GCTTGGATTGAGTTGCTGGAT 3

RESULT 13
US-11-348-413-884139/c
; Sequence 884139, Application US/11348413
; Publication No. US20060160121A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; APPLICANT: Murphy, Ellen
; APPLICANT: Olmsted, Stephen
; TITLE OF INVENTION: PROBE ARRAYS FOR DETECTING MULTIPLE STRAINS OF DIFFERENT SPECIES
; FILE REFERENCE: 031896-084100 (AM 101724)
; CURRENT APPLICATION NUMBER: US/11/348,413
; CURRENT FILING DATE: 2006-02-07
; PRIOR APPLICATION NUMBER: PCT/US05/035471
; PRIOR FILING DATE: 2005-10-05
; PRIOR APPLICATION NUMBER: US 11/243,445
; PRIOR FILING DATE: 2005-10-05
; PRIOR APPLICATION NUMBER: US 60/615,573
; PRIOR FILING DATE: 2004-10-05
; NUMBER OF SEQ ID NOS: 1276209
; SEQ ID NO 884139
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: probe
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(25)
; OTHER INFORMATION: SEQ ID NO: 7816; WANO1UMPL_at; Start 185; Stop 209;
; OTHER INFORMATION: 00000010000000
US-11-348-413-884139

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Query Match      18.4%; Score 15.6; DB 9; Length 25;
Best Local Similarity 36.4%; Pred. NO. 2.1e+04;
Matches 8: Conservative 10; Mismatches 4; Indels 0; Gaps 0;

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Query Match 18.1%; Score 15.4; DB 9; Length 25;
Best Local Similarity 40.0%; Pred. No. 2.5e+04;
Matches 10; Conservative 9; Mismatches 6; Indels 0; Gaps 0;

QY 52 GCGCUUGCUCUGUUUCUGGAUG 76
DB 25 GAGCTTAACCTTCTGTTCGGCATG 1

Search completed: October 16, 2006, 14:22:02
Job time : 189.534 secs

QY 54 GCUUGCUCUGUUUCUGGAU 75
DB 25 GATTGGCCTCTGTTCCTTGAT 4

RESULT 14
US-11-217-529-98618/c
; Sequence 98618, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 98618
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-98618

Query Match 18.1%; Score 15.4; DB 8; Length 25;
Best Local Similarity 52.0%; Pred. No. 2.5e+04;
Matches 13; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

QY 60 CUUCUGUUUCUGGACAGUCC 84
DB 25 CTTCAAAATTCGACGACAGTGCC 1

RESULT 15
US-11-348-413-350690/c
; Sequence 350690, Application US/11348413
; Publication No. US20060160121A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; APPLICANT: Murphy, Ellen
; APPLICANT: Olmsted, Stephen
; TITLE OF INVENTION: PROBE ARRAYS FOR DETECTING MULTIPLE STRAINS OF DIFFERENT SPECIES
; FILE REFERENCE: 031896-084100 (AM 101724)
; CURRENT APPLICATION NUMBER: US/11/348,413
; CURRENT FILING DATE: 2006-02-07
; PRIOR APPLICATION NUMBER: PCT/US05/035471
; PRIOR FILING DATE: 2005-10-05
; PRIOR APPLICATION NUMBER: US 11/243,445
; PRIOR FILING DATE: 2005-10-05
; PRIOR APPLICATION NUMBER: US 60/615,573
; PRIOR FILING DATE: 2004-10-05
; NUMBER OF SEQ ID NOS: 1276209
; SEQ ID NO 350690
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: probe
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (1)..(25)
; OTHER INFORMATION: SEQ ID NO: 10828; WAN01UOXH; Start 36; Stop 60;
; OTHER INFORMATION: 00000000011101
US-11-348-413-350690

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OM nucleic - nucleic search, using sw model

Run on: October 16, 2006, 13:53:09 ; Search time 125.594 Seconds
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Title: US-10-604-726A-6034
Perfect score: 24
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Searched: 5244920 seqs, 3486124231 residues

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14: Geneseqn2005s.*
15: Geneseqn2006s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES			
Result No.	Score	Query Match Length DB ID	Description
1	15.8	65.8	24 6 ABQ11002
2	15.8	65.8	24 6 ABQ04674
3	15.8	65.8	24 6 ABQ04715
4	15.8	65.8	24 6 ABQ00358
5	15.8	65.8	24 6 ABQ11043
6	15.8	65.8	25 6 ABQ12538
7	15.8	65.8	25 6 ABQ12579
8	15.2	63.3	28 2 AAT74315
9	14.6	60.8	24 6 AAL50117
10	14.4	60.0	21 9 ADA24254
11	14.2	59.2	20 14 ADZ97885
12	14.2	59.2	21 11 ADJ13347
13	14.2	59.2	25 3 AAAG1591
14	14.1	58.3	25 9 ACT82777
15	13.8	57.5	17 8 ACDS7816
16	13.8	57.5	17 12 ADI83268
17	13.8	57.5	22 2 AAT47817
18	13.8	57.5	22 2 AAX04299

19	13.6	56.7	21 14 ACL41634
20	13.6	56.7	21 14 ACL41632
21	13.6	56.7	21 14 ACL43064
22	13.6	56.7	30 14 AED57579
23	13.4	55.8	28 6 ABQ79069
24	13.4	55.8	28 6 ABL50688
25	13.4	55.8	28 10 ADD69148
26	13.4	55.8	30 4 AAS95201
27	13.2	55.0	19 14 AEA25301
28	13.2	55.0	19 14 AEA25458
29	13.2	55.0	20 10 ABZ99113
30	13.2	55.0	20 11 ABD32144
31	13.2	55.0	20 12 ADJ60998
32	13.2	55.0	20 12 ADO46487
33	13.2	55.0	20 14 ADZ97886
34	13.2	55.0	20 14 AED42052
35	13.2	55.0	21 11 ADJ13385
36	13.2	55.0	21 13 ADU43508
37	13.2	55.0	25 5 AAF85432
38	13.2	55.0	25 9 ACK10389
39	13.2	55.0	25 10 AAD64634
40	13.2	55.0	25 12 ADO61007
41	13.2	55.0	25 14 AEC90171
42	13.2	55.0	26 13 ADZ15690
43	13.2	55.0	26 13 ADZ15691
44	13.2	55.0	26 14 ADW95301
45	13.2	55.0	30 2 AAQ89038

ALIGNMENTS

RESULT 1
ABQ11002
ID ABQ11002 standard; DNA; 24 BP.
XX ABQ11002;
AC ABQ11002;
XX
DT 11-JUN-2002 (first entry)
XX
DE Oligonucleotide adapter/capture probe 10993.
XX Oligonucleotide array; adapter sequence; probe; ss.
KW Oligonucleotide array; adapter sequence; probe; ss.
XX Synthetic.
XX WO200216649-A2.
XX 28-FEB-2002.
XX
PF 27-AUG-2001; 2001WO-US026519.
XX
PR 25-AUG-2000; 2000US-0227948P.
PR 29-AUG-2000; 2000US-0228854P.
XX (ILLU-) ILLUMINA INC.
Gunderson K;
WPI; 2002-292068/33.
XX
PT Array comprising adapter sequences useful for immobilizing or detecting a target nucleic acid sequence, has different addresses comprising different specific capture probes.
XX Claim 1; Page 225; 261pp; English.
XX The invention relates to an oligonucleotide array (I) comprising at least 25 different addresses (adapter sequences) with each comprising a different capture probe selected from a group consisting of the sequences given in ABQ00010-ABQ13409. (I) is useful for immobilising a target nucleic acid sequence by attaching a adapter nucleic acid (ABQ00010-ABQ13409) to a target nucleic acid to form a modified target nucleic acid

CC and contacting the modified target nucleic acid with (I). The steps of
CC above method is useful for detecting a target nucleic acid, which further
CC comprises detecting the presence of the modified target nucleic acid
XX
SQ Sequence 24 BP; 7 A; 2 C; 10 G; 5 T; 0 U; 0 Other;
Query Match 65.8%; Score 15.8; DB 6; Length 24;
Best Local Similarity 73.7%; Pred. No. 1.3e+03;
Matches 14; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
OY 2 GAGAGGGCGUGUUAAGGC 20
Db 4 GAGAGGCGTGGTTAAGGC 22
RESULT 2
ID ABQ04674 standard; DNA; 24 BP.
XX ABQ04674;
AC ABQ04674;
XX
XX
DT 11-JUN-2002 (first entry)
XX
XX Oligonucleotide adapter/capture probe 4665.
DE Oligonucleotide array; adapter sequence; probe; ss.
KW
XX
OS Synthetic.
XX
XX WO200216649-A2.
XX
XX 28-FEB-2002.
PD
XX
XX 27-AUG-2001; 2001WO-US026519.
PF
XX
XX 25-AUG-2000; 2000US-0227948P.
PR
XX 29-AUG-2000; 2000US-0228854P.
XX
XX (ILLU-) ILLUMINA INC.
PA
XX
XX Gunderson K;
PI
XX
XX WPI; 2002-292068/33.
DR
XX
XX Array comprising adapter sequences useful for immobilizing or detecting a
PT target nucleic acid sequence, has different addresses comprising
PT different specific capture probes.
XX
XX Claim 1; Page 147; 261pp; English.
PS
XX
XX The invention relates to an oligonucleotide array (I) comprising at least
CC 25 different addresses (adapter sequences) with each comprising a
CC different capture probe selected from a group consisting of the sequences
CC given in ABQ00010-ABQ13409. (I) is useful for immobilising a target
CC nucleic acid sequence by attaching a adapter nucleic acid (ABQ00010-
CC ABQ13409) to a target nucleic acid to form a modified target nucleic acid
CC and contacting the modified target nucleic acid with (I). The steps of
CC above method is useful for detecting a target nucleic acid, which further
CC comprises detecting the presence of the modified target nucleic acid
XX
XX Sequence 24 BP; 7 A; 2 C; 10 G; 5 T; 0 U; 0 Other;
Query Match 65.8%; Score 15.8; DB 6; Length 24;
Best Local Similarity 73.7%; Pred. No. 1.3e+03;
Matches 14; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
OY 2 GAGAGGGCGUGUUAAGGC 20
Db 4 GAGAGGCGTGGTTAAGGC 22
RESULT 3
ID ABQ04715/c

ID ABQ04715 standard; DNA; 24 BP.
XX
XX ABQ04715;
AC
XX
DT 11-JUN-2002 (first entry)
XX
XX Oligonucleotide adapter/capture probe 4706.
DE Oligonucleotide array; adapter sequence; probe; ss.
KW
XX
OS Synthetic.
XX
XX WO200216649-A2.
XX
XX 28-FEB-2002.
PD
XX
XX 27-AUG-2001; 2001WO-US026519.
PF
XX
XX 25-AUG-2000; 2000US-0227948P.
PR
XX 29-AUG-2000; 2000US-0228854P.
XX
XX (ILLU-) ILLUMINA INC.
PA
XX
XX Gunderson K;
PI
XX
XX WPI; 2002-292068/33.
DR
XX
XX Array comprising adapter sequences useful for immobilizing or detecting a
PT target nucleic acid sequence, has different addresses comprising
PT different specific capture probes.
XX
XX Claim 1; Page 147; 261pp; English.
PS
XX
XX The invention relates to an oligonucleotide array (I) comprising at least
CC 25 different addresses (adapter sequences) with each comprising a
CC different capture probe selected from a group consisting of the sequences
CC given in ABQ00010-ABQ13409. (I) is useful for immobilising a target
CC nucleic acid sequence by attaching a adapter nucleic acid (ABQ00010-
CC ABQ13409) to a target nucleic acid to form a modified target nucleic acid
CC and contacting the modified target nucleic acid with (I). The steps of
CC above method is useful for detecting a target nucleic acid, which further
CC comprises detecting the presence of the modified target nucleic acid
XX
XX Sequence 24 BP; 5 A; 10 C; 2 G; 7 T; 0 U; 0 Other;
Query Match 65.8%; Score 15.8; DB 6; Length 24;
Best Local Similarity 73.7%; Pred. No. 1.3e+03;
Matches 14; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
OY 2 GAGAGGGCGUGUUAAGGC 20
Db 21 GAGAGGCGTGGTTAAGGC 3
RESULT 4
ID ABQ00358 standard; DNA; 24 BP.
XX
XX ABQ00358;
AC
XX
XX 11-JUN-2002 (first entry)
DT
XX
XX Oligonucleotide adapter/capture probe 349.
DE
XX
XX Oligonucleotide array; adapter sequence; probe; ss.
KW
XX
OS Synthetic.
XX
XX WO200216649-A2.
XX
XX 28-FEB-2002.
PD
XX
XX 27-AUG-2001; 2001WO-US026519.
PF

XX 25-AUG-2000; 2000US-0227948P.
PR 29-AUG-2000; 2000US-0228854P.
XX (ILLU-) ILLUMINA INC.
XX Gunderson K;
XX WPI; 2002-292068/33.
DR Array comprising adapter sequences useful for immobilizing or detecting a
PT target nucleic acid sequence, has different addresses comprising
PT different specific capture probes.
XX
PS Claim 1; Page 52; 261pp; English.
XX
CC The invention relates to an oligonucleotide array (I) comprising at least
CC 25 different addresses (adapter sequences) with each comprising a
CC different capture probe selected from a group consisting of the sequences
CC given in ABQ00010-ABQ13409. (I) is useful for immobilising a target
CC nucleic acid sequence by attaching a adapter nucleic acid (ABQ00010-
CC ABQ13409) to a target nucleic acid to form a modified target nucleic acid
CC and contacting the modified target nucleic acid with (I). The steps of
CC above method is useful for detecting a target nucleic acid, which further
CC comprises detecting the presence of the modified target nucleic acid
XX
SQ Sequence 24 BP; 7 A; 2 C; 10 G; 5 T; 0 U; 0 Other;
Query Match 65.8%; Score 15.8; DB 6; Length 24;
Best Local Similarity 73.7%; Pred. NO. 1.3e+03;
Matches 14; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
XX
QY 2 GAGAGGGCGUGGUUAGGC 20
DB 4 GAGAGGCGTGGTTAAGGC 22
||||| | :||:|||||
RESULT 5
ABQ11043/c
ID ABQ11043 standard; DNA; 24 BP.
XX
AC ABQ11043;
XX
DT 11-JUN-2002 (first entry)
XX
DE Oligonucleotide adapter/capture probe 11034.
XX
KW Oligonucleotide array; adapter sequence; probe; ss.
XX
OS Synthetic.
XX
PN WO200216649-A2.
XX
PD 28-FEB-2002.
XX
PF 27-AUG-2001; 2001WO-US026519.
XX
PR 25-AUG-2000; 2000US-0227948P.
PR 29-AUG-2000; 2000US-0228854P.
XX
PA (ILLU-) ILLUMINA INC.
XX
PI Gunderson K;
XX
DR WPI; 2002-292068/33.
XX
PT Array comprising adapter sequences useful for immobilizing or detecting a
PT target nucleic acid sequence, has different addresses comprising
PT different specific capture probes.
XX
PS Claim 1; Page 225; 261pp; English.
XX
CC The invention relates to an oligonucleotide array (I) comprising at least

CC 25 different addresses (adapter sequences) with each comprising a
CC different capture probe selected from a group consisting of the sequences
CC given in ABQ00010-ABQ13409. (I) is useful for immobilising a target
CC nucleic acid sequence by attaching a adapter nucleic acid (ABQ00010-
CC ABQ13409) to a target nucleic acid to form a modified target nucleic acid
CC and contacting the modified target nucleic acid with (I). The steps of
CC above method is useful for detecting a target nucleic acid, which further
CC comprises detecting the presence of the modified target nucleic acid
XX
SQ Sequence 24 BP; 5 A; 10 C; 2 G; 7 T; 0 U; 0 Other;
Query Match 65.8%; Score 15.8; DB 6; Length 24;
Best Local Similarity 73.7%; Pred. NO. 1.3e+03;
Matches 14; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
XX
QY 2 GAGAGGGCGUGGUUAGGC 20
DB 21 GAGAGGCGTGGTTAAGGC 3
||||| | :||:|||||
RESULT 6
ABQ12538
ID ABQ12538 standard; DNA; 25 BP.
XX
AC ABQ12538;
XX
DT 11-JUN-2002 (first entry)
XX
DE Oligonucleotide adapter/capture probe 12529.
XX
KW Oligonucleotide array; adapter sequence; probe; ss.
XX
OS Synthetic.
XX
PN WO200216649-A2.
XX
PD 28-FEB-2002.
XX
PF 27-AUG-2001; 2001WO-US026519.
XX
PR 25-AUG-2000; 2000US-0227948P.
PR 29-AUG-2000; 2000US-0228854P.
XX
PA (ILLU-) ILLUMINA INC.
XX
PI Gunderson K;
XX
DR WPI; 2002-292068/33.
XX
PT Array comprising adapter sequences useful for immobilizing or detecting a
PT target nucleic acid sequence, has different addresses comprising
PT different specific capture probes.
XX
PS Claim 1; Page 244; 261pp; English.
XX
CC The invention relates to an oligonucleotide array (I) comprising at least
CC 25 different addresses (adapter sequences) with each comprising a
CC different capture probe selected from a group consisting of the sequences
CC given in ABQ00010-ABQ13409. (I) is useful for immobilising a target
CC nucleic acid sequence by attaching a adapter nucleic acid (ABQ00010-
CC ABQ13409) to a target nucleic acid to form a modified target nucleic acid
CC and contacting the modified target nucleic acid with (I). The steps of
CC above method is useful for detecting a target nucleic acid, which further
CC comprises detecting the presence of the modified target nucleic acid
XX
SQ Sequence 25 BP; 7 A; 2 C; 10 G; 6 T; 0 U; 0 Other;
Query Match 65.8%; Score 15.8; DB 6; Length 25;
Best Local Similarity 73.7%; Pred. NO. 1.3e+03;
Matches 14; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
XX
QY 2 GAGAGGGCGUGGUUAGGC 20
||||| | :||:|||||

```
Db          5 GAGAGGCGTTGGTTAAGGC 23

RESULT 7
ABQ12579/c
ID ABQ12579 standard; DNA; 25 BP.
XX
AC ABQ12579;
XX
DT 11-JUN-2002 (first entry)
XX
DE Oligonucleotide adapter/capture probe 12570.
XX
KW Oligonucleotide array; adapter sequence; probe; ss.
OS Synthetic.
XX
XX WO200216649-A2.
XX
PD 28-FEB-2002.
XX
PF 27-AUG-2001; 2001WO-US026519.
XX
PR 25-AUG-2000; 2000US-0227948P.
XX
PR 29-AUG-2000; 2000US-0228854P.
XX
XX (ILLU-) ILLUMINA INC.
XX
XX Gunderson K;
XX
XX WPI; 2002-292068/33.
XX
XX Array comprising adapter sequences useful for immobilizing or detecting a
PT target nucleic acid sequence, has different addresses comprising
PT different specific capture probes.
XX
XX Claim 1; Page 244; 261pp; English.
XX
XX The invention relates to an oligonucleotide array (I) comprising at least
CC 25 different addresses (adapter sequences) with each comprising a
CC different capture probe selected from a group consisting of the sequences
CC given in ABQ00010-ABQ13409. (I) is useful for immobilising a target
CC nucleic acid sequence by attaching a adapter nucleic acid (ABQ00010-
CC ABQ13409) to a target nucleic acid to form a modified target nucleic acid
CC and contacting the modified target nucleic acid with (I). The steps of
CC above method is useful for detecting a target nucleic acid, which further
CC comprises detecting the presence of the modified target nucleic acid
XX
XX Sequence 25 BP; 5 A; 10 C; 2 G; 8 T; 0 U; 0 Other;

Query Match 65.8%; Score 15.8; DB 6; Length 25;
Best Local Similarity 73.7%; Pred. No. 1.3e+03;
Matches 14; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 2 GAGAGGCGCGUGUUAAGGC 20
    ||||| | : : : : |||||
Db 22 GAGAGGCGTTGGTTAAGGC 4

RESULT 8
AAT74315/c
ID AAT74315 standard; DNA; 28 BP.
XX
AC AAT74315;
XX
XX 09-FEB-1998 (first entry)
XX
DE PCR primer JC25.2.
XX
XX Cleaning; bleaching; cellulose; fabric; enzyme hybrid; peroxidase;
KW cellulose binding domain; Humicola insolens; cellulase;
KW Coprinus cinereus; laccase; plasmid pJC25; PCR; primer; ss.
XX

Db          5 GAGAGGCGTTGGTTAAGGC 23

RESULT 9
AAL50117/c
ID AAL50117 standard; DNA; 24 BP.
XX
AC AAL50117;
XX
XX 28-JAN-2003 (first entry)
XX
DE Human CAB555953-1 ligand binding domain PCR primer #2.
XX
XX Human; CAB555953.1; nuclear hormone receptor ligand binding domain; LBDG3;
KW cancer; autoimmune disorder; inflammation; PCR; antiseborrheic;
KW dermatological; anti-HIV; neuroprotective; nephrotropic; antianginal;
KW tranquilizer; antiarrhythmic; antiarteriosclerotic; antiaesthetic;
KW immunosuppressive; virucide; fungicide; antibacterial; antiparasitic;
KW cardiant; antidepressant; antidiabetic; vasotropic; antiinflammatory;
KW nephrotropic; cytostatic; antilipemic; hypotensive; antiallergic;
KW antithyroid; anorectic; osteopathic; analgesic; antipsoriatic; vulnery;
KW cerebroprotective; haemostatic; thrombolytic; cardiovascular disorder;
KW neurological disorder; infection; primer; ss.
XX
XX Homo sapiens.
XX
XX WO200270557-A2.
XX
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PD 12-SEP-2002.
XX
PF 05-MAR-2002; 2002WO-GB000937.
XX
PR 05-MAR-2001; 2001GB-00005402.
XX
XX (INPH-) INPHARMATICA LTD.
XX
XX Fagan RJ, Phelps CB, Phillips T, Pierron VN, Allen KE, Allen JM;
PI Potter SJ;
XX
XX WPI; 2002-698731/75.
XX
XX New CAB55953.1 or LBDG3 polypeptide, useful as a nuclear hormone receptor
PT ligand-binding domain, or for manufacturing of a medicament for
PT diagnosing or treating cell proliferative disorders or
PT autoimmune/inflammatory disorders.
XX
XX Example 2; Page 64; 122pp; English.
XX
CC The present invention relates to the protein and coding sequences of a
CC human nuclear hormone receptor ligand binding domain designated
CC CAB55953.1 or LBDG3. The sequences are useful in the treatment of cancer,
CC autoimmune/inflammatory disorders, including allergy, inflammatory bowel
CC disease, arthritis, psoriasis and respiratory tract inflammation, asthma
CC and organ transplant rejection, cardiovascular disorders, including
CC hypertension, oedema, angina, atherosclerosis, thrombosis, sepsis, shock,
CC reperfusion injury, heart arrhythmia, and ischaemia, neurological
CC disorders including central nervous system disease, Alzheimer's disease,
CC brain injury, stroke, amyotrophic lateral sclerosis, anxiety, depression
CC and pain, developmental disorders, metabolic disorders including diabetes
CC mellitus, osteoporosis, lipid metabolism disorders, hyperthyroidism,
CC hyperparathyroidism, hypercalcaemia, hypercholesterolaemia,
CC hyperlipidaemia and obesity, renal disorders including
CC glomerulonephritis, renovascular hypertension, dermatological disorders
CC including acne, eczema and wound healing, negative effects of aging,
CC acquired immunodeficiency syndrome (AIDS), viral, bacterial, fungal and
CC parasitic infections, and other pathological conditions, particularly
CC those in which nuclear hormone receptors are implicated. The present
CC sequence is a PCR primer used to isolate the coding sequence of the
CC invention
XX
XX Sequence 24 BP; 7 A; 7 C; 4 G; 6 T; 0 U; 0 Other;
SQ
Query Match 60.8%; Score 14.6; DB 6; Length 24;
Best Local Similarity 61.9%; Pred. No. 4.8e+03;
Matches 13; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 3 AGAGGGCGUGGUUAGCGCUC 23
DB 23 AGAGGGGCTTATTAACTCGTC 3

RESULT 10
ADA24254/c
ID ADA24254 standard; DNA; 21 BP.
XX
XX ADA24254;
XX
XX 20-NOV-2003 (first entry)
XX
XX Major allergenic storage protein FAGAG1 PCR primer FAG19 SEQ ID NO:7.
XX food testing; allergen; PCR primer; Fagopyrum esculentum;
XX major allergenic storage protein; FAGAG1; ss.
XX
XX Synthetic.
XX Fagopyrum esculentum.
XX
XX WO2003068964-A1.
XX
XX 21-AUG-2003.
XX
```

```
PF 26-SEP-2002; 2002WO-JP009982.
XX
PR 15-FEB-2002; 2002JP-00038930.
XX
PA (NISS ) NISSHIN SEIFUN GROUP INC.
XX
XX Yamakawa H, Suzuki E, Miyatake K, Hayakawa K;
PI WPI; 2003-637145/60.
XX
XX PCR-based method for testing foods using specific primers designed from
PT genes of target substance, useful in detecting trace components or
PT identifying specific harmful allergens in (processed) foods.
XX
XX Disclosure; Page 10; 38pp; Japanese.
XX
CC The present invention describes a method for testing the presence or
CC absence of a specific substance in a food by performing PCR with primers
CC which are designed on the basis of data obtained from a part of a gene of
CC the specific substance. Also described: (1) a similar method for
CC detecting a trace component contained in a food, or for identifying a
CC harmful allergen specific to a consumer of such substance by performing
CC PCR with primers which are designed on the basis of data obtained from a
CC part of a gene of the specific substance; (2) primers for PCR applicable
CC in food testing which are designed on the basis of data obtained from a
CC part of a gene of the specific substance; and (3) kits for determining
CC concentration of a specific substance in the food containing the primers.
CC The methods are useful for testing foods, which can be used in detecting
CC trace components or identifying specific harmful allergens in (processed)
CC foods, particularly applicable in food safety and management. The present
CC sequence represents a PCR primer for a Fagopyrum esculentum major
CC allergenic storage protein designated FAGAG1, which is used in the
CC exemplification of the present invention.
XX
XX Sequence 21 BP; 7 A; 8 C; 3 G; 3 T; 0 U; 0 Other;
SQ
Query Match 60.0%; Score 14.4; DB 9; Length 21;
Best Local Similarity 68.8%; Pred. No. 5.9e+03;
Matches 11; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 7 GGGCGUGGUUAGCGCU 22
DB 17 GGGCTGGTTATGCGCT 2

RESULT 11
ADZ97885/c
ID ADZ97885 standard; DNA; 20 BP.
XX
XX ADZ97885;
XX
XX 28-JUL-2005 (first entry)
XX
XX Human antisense oligonucleotide SEQ ID NO:39.
XX protein interaction; antisense oligonucleotide; ss.
XX
XX Homo sapiens.
XX
XX US2005112118-A1.
XX
XX 26-MAY-2005.
XX
XX 20-OCT-2003; 2003US-00690276.
XX
XX 02-DEC-1999; 99US-0168377P.
XX 02-DEC-1999; 99US-0168379P.
XX 25-FEB-2000; 2000US-0185056P.
XX 01-DEC-2000; 2000US-00727384.
XX 14-DEC-2000; 2000US-0255063P.
XX 21-DEC-2000; 2000US-0256986P.
XX 04-JAN-2001; 2001US-0259571P.
XX 04-JAN-2001; 2001US-0259572P.
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PT Trypsin family serine proteases expressed specifically in mature testis
PT for development of methods for diagnosis and treatment of sterility and
PT for contraception.

XX Example 9; Page 45; 121pp; Japanese.

XX The invention relates to novel murine and human testis specific serine
CC proteases (Tespac PRO; AAB03156-B03160) and to cDNAs encoding them
CC (AAA61558-A61562). It also encompasses expression vectors and host cells
CC comprising a nucleotide sequence encoding a protease of the invention,
CC inhibitors of the proteases and antibodies against the proteases. The
CC novel proteases are members of the trypsin family of serine proteases,
CC having the serine and histidine active site signatures characteristic of
CC this family. The proteases are specifically expressed in mature testis
CC and participate in the differentiation and maturation of sperm. The
CC proteases are potentially useful for the development of pharmaceuticals
CC for the treatment of male infertility and other male reproductive
CC disorders, and for the development of contraceptives. They may also be
CC used as reagents for the diagnosis of male infertility. Sequences
CC AAA61590-A61593 represent RACE (rapid amplification of cDNA ends) PCR
CC primers used in the isolation of cDNA encoding human Tespec PRO-3
CC (AAA61561)

SQ Sequence 25 BP; 4 A; 2 C; 10 G; 9 T; 0 U; 0 Other;

Query Match 59.2%; Score 14.2; DB 3; Length 25;
Best Local Similarity 63.2%; Pred. No. 7.4e+03;
Matches 12; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

OY 4 GAGGGCGUGGUUAGGCGU 22
||| ||| : : : : :
DB 3 GATGGCTAGTTAAGTCGT 21

RESULT 14

AC182777

ID AC182777 standard; DNA; 25 BP.

XX AC

AC AC182777;

DT 14-OCT-2003 (first entry)

XX Human microarray DNA oligonucleotide SEQ ID NO 82769.

XX EST; ss; probe; expressed sequence tag; microarray; gene expression;
KW genetic variation; biallelic marker; polymorphism; human;
KW cross-species comparison.

XX Homo sapiens.

OS US2003104410-A1.

XX 05-JUN-2003.

XX 15-MAR-2002; 2002US-00098263.

XX 16-MAR-2001; 2001US-0276759P.

XX (AFFY-) AFFYMETRIX INC.

XX Mittmann MP;

XX WPI; 2003-567953/53.

XX New array of nucleic acid probes, useful for in situ hybridization, in
PT Southern, Northern or dot-blot hybridization to identify or detect the
PT sequence or specific mutations of any gene.

XX Claim 1; SEQ ID NO 82768; 9pp; English.

XX The invention discloses a microarray comprising a plurality of nucleic
CC acid probes including one of 2,018,500 fully defined sequences, or its
CC perfect match, perfect mismatch, antisense match or antisense mismatch.

CC Also disclosed is a method of gene expression analysis. The array is used
CC in monitoring gene expression levels by hybridisation to a DNA library,
CC in analysis of genetic variation or in hybridisation of tag-labelled
CC compounds. The nucleic acid probes are specifically designed for analysis
CC of at least one target sequence. The method of analysis comprises
CC hybridising at least one or more nucleic acids to at least two or more
CC nucleic acid probes and detecting the hybridisation. The nucleic acid
CC probes are attached to a solid support. The analysis comprises monitoring
CC gene expression levels, identifying biallelic markers or polymorphisms,
CC or family members of a gene and a cross-species comparison. Each of the
CC nucleic acids further comprises a tag sequence. The array of nucleic acid
CC probes is useful in in situ hybridisation, in Southern, Northern or dot-
CC blot hybridisation to identify or detect the sequence or specific
CC mutations of any gene, in mapping the 5' termini of mRNA molecules by
CC primer extensions or in screening cDNA or genomic libraries or subclones
CC for additional subclones containing segments of DNA that have been
CC isolated and previously sequenced. The sequence presented is one of the
CC nucleic acid probes incorporated in the microarray. Note: The sequence
CC data for this patent can also be obtained in electronic format directly
CC from USPTO at seqdata.uspto.gov/sequence.html
XX
SQ Sequence 25 BP; 6 A; 4 C; 10 G; 5 T; 0 U; 0 Other;

Query Match 58.3%; Score 14; DB 9; Length 25;

Best Local Similarity 59.1%; Pred. No. 9.2e+03;

Matches 13; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

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RESULT 15

ACD57816/C

ID ACD57816 standard; RNA; 17 BP.

XX AC

AC ACD57816;

DT 23-SEP-2003 (first entry)

XX HCV DNAzyme substrate sequence #514.

XX Nucleic acid molecule; Hepatitis C virus; HCV; Hepatitis B virus; HBV;
KW RNA stability; RNA expression; RNA synthesis; antisense;
KW enzymatic nucleic acid; hammerhead ribozyme; DNAzyme; inozyme; zinzyme;
KW amberyyme; G-cleaver ribozyme; decoy molecule; aptamer;
KW HBV reverse transcriptase; Enhancer I region; viral replication;
KW degenerative; disease state; HBV infection; HCV infection; cirrhosis;
KW liver failure; hepatocellular carcinoma; hepatotropic; cytostatic;
KW virucide; antiinflammatory; substrate; ss.

OS Hepatitis C virus.

XX WO200281494-A1.

XX 17-OCT-2002.

XX 26-MAR-2002; 2002WO-US009187.

XX 26-MAR-2001; 2001US-00817879.

XX 08-JUN-2001; 2001US-00877478.

XX 08-JUN-2001; 2001US-0296876P.

XX 24-OCT-2001; 2001US-033059P.

XX 05-DEC-2001; 2001US-0337055P.

XX (RIBO-) RIBOZYME PHARM INC.

XX (BLAT/) BLATT L.

XX (MACE/) MACEJAK D.

XX (MCSW/) MCSWIGGEN J.

XX (MORR/) MORRISSEY D.

XX (PAVC/) PAVCO P.

XX (LEEP/) LEE P.

XX (DRAP/) DRAPER K.

PA (ROBE/) ROBERTS E.
XX
PI Blatt L, Macejak D, Mcswiggen J, Morrissey D, Pavco P, Lee P;
PI Draper K, Roberts E;
XX
DR WPI; 2003-229207/22.
XX
XX Novel compound useful for treating cirrhosis, liver failure,
PT hepatocellular carcinoma, or condition associated with hepatitis C virus
PT infection.
XX
XX Claim 1; Page 243; 387pp; English.
PS
XX The present invention relates to nucleic acid molecules which modulate
CC the synthesis, expression and/or stability of Hepatitis C virus (HCV) or
CC Hepatitis B virus (HBV) RNA. The nucleic acid molecules include antisense
CC and enzymatic nucleic acids such as hammerhead ribozymes, DNazymes,
CC inozymes, zinzymes, ambezymes, and G-cleaver ribozymes. Also disclosed
CC are nucleic acid decoy molecules and aptamers that bind to HBV reverse
CC transcriptase and/or HBV reverse transcriptase primer sequences, as well
CC as oligonucleotides that specifically bind the Enhancer I region of HBV
CC DNA. The nucleic acids may be used to modulate the expression of HBV
CC genes and HBV viral replication. Also disclosed is a method for screening
CC compounds and/or potential therapies directed against HBV, and compounds
CC that modulate the expression and/or replication of HCV. The compounds and
CC methods of the invention are useful for the treatment of degenerative and
CC disease states related to HBV and HCV infection, replication and gene
CC expression such as cirrhosis, liver failure, and hepatocellular
CC carcinoma. The present sequence represents a substrate for one of the HCV
CC DNazyme or minus strand DNazyme sequences disclosed in the present
XX invention
XX
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Query Match 57.5%; Score 13.8; DB 8; Length 17;
Best Local Similarity 70.6%; Pred. No. 1.1e+04;
Matches 12; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 6 GGGGCGUGGUUAGGCGU 22
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Db 17 GGGGCAGGTTAAGGTGT 1

Search completed: October 16, 2006, 14:15:57
Job time : 126.594 secs

GenCore version 5.1.9

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OM nucleic - nucleic search, using sw model

Run on: October 16, 2006, 13:57:30 ; Search time 590.797 Seconds

(without alignments)

2597.742 Million cell updates/sec

Title: US-10-604-726A-6034

Perfect score: 24

Sequence: 1 ugagagggcguguaagcgucc 24

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 6366136 seqs, 31973710525 residues

Total number of hits satisfying chosen parameters: 1796954

Minimum DB seq length: 0

Maximum DB seq length: 30

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl:

- 1: gb_env:*
- 2: gb_pat:*
- 3: gb_ph:*
- 4: gb_pl:*
- 5: gb_pr:*
- 6: gb_ro:*
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- 8: gb_sy:*
- 9: gb_un:*
- 10: gb_vi:*
- 11: gb_ov:*
- 12: gb_htg:*
- 13: gb_in:*
- 14: gb_om:*
- 15: gb_ba:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	15.8	65.8	24	2	AX443910 Sequence
2	15.8	65.8	25	2	AX447886 Sequence
3	14.6	60.8	24	2	AX538707 Sequence
4	13.8	57.5	22	2	AR036420 Sequence
5	13.8	57.5	22	2	I29861 Sequence 12
6	13.4	55.8	28	2	BD141786 Novel G p
7	13.4	55.8	28	2	BD173668 Novel phy
8	13.4	55.8	28	2	BD181737 Novel G p
9	13.2	55.0	25	2	AR148541 Sequence
10	13.2	55.0	25	2	I62320 Sequence 23
11	13	54.2	17	2	AX215297 Sequence
12	13	54.2	17	2	AX215298 Sequence
13	13	54.2	17	2	AX215299 Sequence
14	13	54.2	17	2	AX215300 Sequence
15	13	54.2	20	2	AX298773 Sequence
16	13	54.2	27	2	AX347840 Sequence
17	12.8	53.3	19	2	AR069252 Sequence
18	12.8	53.3	19	2	CS101953 Sequence

19	12.8	53.3	19	2	CS102090	CS102090 Sequence
20	12.8	53.3	25	2	AR240243	AR240243 Sequence
21	12.6	52.5	19	2	AR628705	AR628705 Sequence
22	12.6	52.5	20	2	AR100388	AR100388 Sequence
23	12.6	52.5	20	2	AR150043	AR150043 Sequence
24	12.6	52.5	20	2	BD227916	BD227916 Antisense
25	12.6	52.5	20	2	AR442443	AR442443 Sequence
26	12.6	52.5	20	8	AB213914	AB213914 Synthetic
27	12.6	52.5	21	2	AR231257	AR231257 Sequence
28	12.6	52.5	22	2	CS020856	CS020856 Sequence
29	12.6	52.5	25	2	AR404657	AR404657 Sequence
30	12.6	52.5	26	5	S75471	S75471 rhodopsin {
31	12.6	52.5	27	2	DD210483	DD210483 GENOMIC S
32	12.6	52.5	28	2	AR534679	AR534679 Sequence
33	12.6	52.5	28	2	AX004269	AX004269 Sequence
34	12.6	52.5	30	2	AR139887	AR139887 Sequence
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36	12.6	52.5	30	2	AR167531	AR167531 Sequence
37	12.6	52.5	30	2	AR167568	AR167568 Sequence
38	12.6	52.5	30	2	AX924030	AX924030 Sequence
39	12.6	52.5	30	2	BD084559	BD084559 Recombina
40	12.6	52.5	30	2	BD084596	BD084596 Recombina
41	12.6	52.5	30	2	BD250400	BD250400 Methods f
42	12.6	52.5	30	2	AR234255	AR234255 Sequence
43	12.6	52.5	30	2	AR234292	AR234292 Sequence
44	12.6	52.5	30	2	AR238589	AR238589 Sequence
45	12.6	52.5	30	2	AR476172	AR476172 Sequence

ALIGNMENTS

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DEFINITION	AX443910					
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VERSION						
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SOURCE	synthetic construct					
ORGANISM	other sequences; artificial sequences.					
REFERENCE	1					
AUTHORS	Gunderson,K.					
TITLE	Probes and decoder oligonucleotides					
JOURNAL	Patent: WO 0216649-A 365 28-FEB-2002;					
FEATURES	Illumina, Inc. (US)					
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SOURCE				
ORGANISM				

other sequences; artificial sequences.		/mol_type="unassigned DNA"	
REFERENCE	1	ORIGIN	
AUTHORS	Gunderson,K.	Query Match	57.5%; Score 13.8; DB 2; Length 22;
TITLE	Probes and decoder oligonucleotides	Best Local Similarity	70.6%; Pred. No. 5.4e+05;
JOURNAL	Patent: WO 0216649-A 4341 28-FEB-2002;	Matches	12; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
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Other sequences; artificial sequences.			
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AUTHORS	Fagan,R.J., Phelps,C.B., Phillips,T., Pierron,V.N., Allen,K.E.,		
	Allen,J.M. and Potter,S.J.		
TITLE	Nuclear hormone receptor ligand binding domain		
JOURNAL	Patent: WO 02070557-A 6 12-SEP-2002;		
	Inpharmatica Limited (GB)		
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VERSION			
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REFERENCE			
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AUTHORS	Seizinger,B.R., Kley,N.A. and Bianchi,A.B.		
TITLE	NF2 isoforms		
JOURNAL	Patent: US 5872214-A 12 16-FEB-1999;		
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other sequences; artificial sequences.		/mol_type="unassigned DNA"	
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AUTHORS	Gunderson,K.	Query Match	57.5%; Score 13.8; DB 2; Length 22;
TITLE	Probes and decoder oligonucleotides	Best Local Similarity	70.6%; Pred. No. 5.4e+05;
JOURNAL	Patent: WO 0216649-A 4341 28-FEB-2002;	Matches	12; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
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AUTHORS	Fagan,R.J., Phelps,C.B., Phillips,T., Pierron,V.N., Allen,K.E.,		
	Allen,J.M. and Potter,S.J.		
TITLE	Nuclear hormone receptor ligand binding domain		
JOURNAL	Patent: WO 02070557-A 6 12-SEP-2002;		
	Inpharmatica Limited (GB)		
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1 (bases 1 to 22)			
AUTHORS	Seizinger,B.R., Kley,N.A. and Bianchi,A.B.		
TITLE	NF2 isoforms		
JOURNAL	Patent: US 5872214-A 12 16-FEB-1999;		
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AUTHORS	Gunderson,K.	Query Match	57.5%; Score 13.8; DB 2; Length 22;
TITLE	Probes and decoder oligonucleotides	Best Local Similarity	70.6%; Pred. No. 5.4e+05;
JOURNAL	Patent: WO 0216649-A 4341 28-FEB-2002;	Matches	12; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
FEATURES	Illumina, Inc. (US)		
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Best Local Similarity	73.7%; Pred. No. 6.1e+04;		
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Other sequences; artificial sequences.			
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AUTHORS	Fagan,R.J., Phelps,C.B., Phillips,T., Pierron,V.N., Allen,K.E.,		
	Allen,J.M. and Potter,S.J.		
TITLE	Nuclear hormone receptor ligand binding domain		
JOURNAL	Patent: WO 02070557-A 6 12-SEP-2002;		
	Inpharmatica Limited (GB)		
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1 (bases 1 to 22)			
AUTHORS	Seizinger,B.R., Kley,N.A. and Bianchi,A.B.		
TITLE	NF2 isoforms		
JOURNAL	Patent: US 5872214-A 12 16-FEB-1999;		
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AUTHORS	Gunderson,K.	Query Match	57.5%; Score 13.8; DB 2; Length 22;
TITLE	Probes and decoder oligonucleotides	Best Local Similarity	70.6%; Pred. No. 5.4e+05;
JOURNAL	Patent: WO 0216649-A 4341 28-FEB-2002;	Matches	12; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
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AUTHORS	Fagan,R.J., Phelps,C.B., Phillips,T., Pierron,V.N., Allen,K.E.,		
	Allen,J.M. and Potter,S.J.		
TITLE	Nuclear hormone receptor ligand binding domain		
JOURNAL	Patent: WO 02070557-A 6 12-SEP-2002;		
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1 (bases 1 to 22)			
AUTHORS	Seizinger,B.R., Kley,N.A. and Bianchi,A.B.		
TITLE	NF2 isoforms		
JOURNAL	Patent: US 5872214-A 12 16-FEB-1999;		
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other sequences; artificial sequences.		/mol_type="unassigned DNA"	
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AUTHORS	Gunderson,K.	Query Match	57.5%; Score 13.8; DB 2; Length 22;
TITLE	Probes and decoder oligonucleotides	Best Local Similarity	70.6%; Pred. No. 5.4e+05;
JOURNAL	Patent: WO 0216649-A 4341 28-FEB-2002;	Matches	12; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
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AUTHORS	Fagan,R.J., Phelps,C.B., Phillips,T., Pierron,V.N., Allen,K.E.,		
	Allen,J.M. and Potter,S.J.		
TITLE	Nuclear hormone receptor ligand binding domain		
JOURNAL	Patent: WO 02070557-A 6 12-SEP-2002;		
	Inpharmatica Limited (GB)		
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1 (bases 1 to 22)			
AUTHORS	Seizinger,B.R., Kley,N.A. and Bianchi,A.B.		
TITLE	NF2 isoforms		
JOURNAL	Patent: US 5872214-A 12 16-FEB-1999;		
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AUTHORS	Gunderson,K.	Query Match	57.5%; Score 13.8; DB 2; Length 22;
TITLE	Probes and decoder oligonucleotides	Best Local Similarity	70.6%; Pred. No. 5.4e+05;
JOURNAL	Patent: WO 0216649-A 4341 28-FEB-2002;	Matches	12; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
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ORIGIN					
Query Match 55.8%; Score 13.4; DB 2; Length 28;					
Best Local Similarity 60.9%; Pred. No. 7.9e+05;					
Matches 14; Conservative 3; Mismatches 6; Indels 0; Gaps 0;					
QY	1 UGAGAGGGCGUGUUAAGGCUGC 23 : :: ::				
Db	6 TGAGAGGTGCTGTGCAAGTCTTC 28 : :: ::				
RESULT 7					
LOCUS	BD173668 28 bp DNA linear PAT 18-FEB-2003				
DEFINITION	Novel physiologically active peptide and use thereof.				
ACCESSION	BD173668				
VERSION	BD173668.1 GI:28414999				
KEYWORDS	WO 02062996-A/23. synthetic construct other sequences; artificial sequences.				
ORGANISM	OS Artificial Sequence FN WO 02062996-A/23				
REFERENCE					
AUTHORS	Otake,T., Masuda,Y. and Takatsu,Y.				
TITLE	Novel physiologically active peptide and use thereof				
JOURNAL	Patent: WO 02062996-A 23 15-AUG-2002; TAKEDA CHEMICAL INDUSTRIES LTD,TETSUYA OTAKI,YASUSHI MASUDA, YOSHIIRO TAKATSU				
COMMENT					
PN	PD 15-AUG-2002				
PF	PD 01-FEB-2002 WO 2002JP000837				
PR	PD 02-FEB-2001 JP 01P 026798				
PI	TETSUYA OTAKI,YASUSHI MASUDA,YOSHIIRO TAKATSU PC				
C12N15/12,C12N1/15,C12N1/19,C12N1/21,C12N5/10,C12P21/02,C07K14/PC					
47,					
PC	C07K16/18,A61K45/00,A61P1/00,G01N33/15,G01N33/50,G01N33/53,PC C12P21/08				
CC	Novel physiologically active peptide and use thereof FH Key				
FT source	1..28 /organism='Artificial Sequence'. Location/Qualifiers				
FT					
FEATURES					
source	1..28 /organism='synthetic construct' /mol_type='genomic DNA' /db_xref='taxon:32630'				
ORIGIN					
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Best Local Similarity 60.9%; Pred. No. 7.9e+05;					
Matches 14; Conservative 3; Mismatches 6; Indels 0; Gaps 0;					
QY	1 UGAGAGGGCGUGUUAAGGCUGC 23 : :: ::				
Db	6 TGAGAGGTGCTGTGCAAGTCTTC 28 : :: ::				
RESULT 9					
LOCUS	AR148541/c 25 bp DNA linear PAT 08-AUG-2001				
DEFINITION	Sequence 23 from patent US 6225115.				
ACCESSION	AR148541				
VERSION	AR148541.1 GI:15112631				
KEYWORDS	Unknown.				
SOURCE	Unknown. Unclassified.				
ORGANISM					
REFERENCE	1 (bases 1 to 25)				
AUTHORS	Smith,K.E., Borden,L.A., Weinshank,R.L. and Hartig,P.R.				
TITLE	DNA encoding taurine and GABA transporters and uses thereof				
JOURNAL	Patent: US 6225115-A 23 01-MAY-2001; Location/Qualifiers				
FEATURES	1..25 /organism='unknown' /mol_type='unassigned DNA'				
source					
ORIGIN					
Query Match 55.0%; Score 13.2; DB 2; Length 25;					
Best Local Similarity 66.7%; Pred. No. 1e+06;					
Matches 12; Conservative 3; Mismatches 3; Indels 0; Gaps 0;					
QY	5 AGGGCGUGGUAAAGCGCU 22 : :: ::				
Db	23 AGGTGCTGTGAAGGCAT 6 : :: ::				
RESULT 10					
LOCUS	I62320/c 25 bp DNA linear PAT 07-OCT-1997				
DEFINITION	Sequence 23 from patent US 5658786.				
ACCESSION	I62320				

VERSION I62320.1 GI:2480268
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 25)
AUTHORS Smith,K.E., Weinschenk,R.L., Borden,L.A. and Hartig,P.R.
TITLE DNA encoding rat taurine transporter and uses thereof
JOURNAL Patent: US 5658786-A 23 19-AUG-1997;
FEATURES Location/Qualifiers
source 1..25
/organism="unknown"
/mol_type="unassigned DNA"
ORIGIN
Query Match 55.0%; Score 13.2; DB 2; Length 25;
Best Local Similarity 66.7%; Pred. No. 1e+06;
Matches 12; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
QY 5 AGGGGCGGUGUAGGCGU 22
Db 23 AGGTGCTGGTGAAGGCAT 6
RESULT 11
AX215297/c
LOCUS AX215297 17 bp RNA linear PAT 07-SEP-2001
DEFINITION Sequence 739 from Patent WO0159103.
ACCESSION AX215297
VERSION AX215297.1 GI:15525340
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1
AUTHORS Blatt,L., McSwiggen,J. and Chowrira,B.M.
TITLE Method and reagent for the modulation and diagnosis of cd20 and nogo gene expression
JOURNAL Patent: WO 0159103-A 739 16-AUG-2001;
RIBOZYME PHARMACEUTICALS, INC. (US) ; Blatt, Lawrence (US) ; McSwiggen, James (US) ; Chowrira, Bharat M. (US)
FEATURES Location/Qualifiers
source 1..17
/organism="synthetic construct"
/mol_type="unassigned RNA"
/db_xref="taxon:32630"
/note="Nucleic Acid"
ORIGIN
Query Match 54.2%; Score 13; DB 2; Length 17;
Best Local Similarity 84.6%; Pred. No. 1.4e+06;
Matches 11; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 1 UGAGAGGGGCGUG 13
Db 16 TGAGAGGGGCTGG 4
RESULT 12
AX215298/c
LOCUS AX215298 17 bp RNA linear PAT 07-SEP-2001
DEFINITION Sequence 740 from Patent WO0159103.
ACCESSION AX215298
VERSION AX215298.1 GI:15525341
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1
AUTHORS Blatt,L., McSwiggen,J. and Chowrira,B.M.
TITLE Method and reagent for the modulation and diagnosis of cd20 and nogo gene expression
JOURNAL Patent: WO 0159103-A 740 16-AUG-2001;
RIBOZYME PHARMACEUTICALS, INC. (US) ; Blatt, Lawrence (US) ; McSwiggen, James (US) ; Chowrira, Bharat M. (US)

RIBOZYME PHARMACEUTICALS, INC. (US) ; Blatt, Lawrence (US) ; McSwiggen, James (US) ; Chowrira, Bharat M. (US)
FEATURES Location/Qualifiers
source 1..17
/organism="synthetic construct"
/mol_type="unassigned RNA"
/db_xref="taxon:32630"
/note="Nucleic Acid"
ORIGIN
Query Match 54.2%; Score 13; DB 2; Length 17;
Best Local Similarity 84.6%; Pred. No. 1.4e+06;
Matches 11; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 1 UGAGAGGGGCGUG 13
Db 15 TGAGAGGGGCTGG 3
RESULT 13
AX215299/c
LOCUS AX215299 17 bp RNA linear PAT 07-SEP-2001
DEFINITION Sequence 741 from Patent WO0159103.
ACCESSION AX215299
VERSION AX215299.1 GI:15525342
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1
AUTHORS Blatt,L., McSwiggen,J. and Chowrira,B.M.
TITLE Method and reagent for the modulation and diagnosis of cd20 and nogo gene expression
JOURNAL Patent: WO 0159103-A 741 16-AUG-2001;
RIBOZYME PHARMACEUTICALS, INC. (US) ; Blatt, Lawrence (US) ; McSwiggen, James (US) ; Chowrira, Bharat M. (US)
FEATURES Location/Qualifiers
source 1..17
/organism="synthetic construct"
/mol_type="unassigned RNA"
/db_xref="taxon:32630"
/note="Nucleic Acid"
ORIGIN
Query Match 54.2%; Score 13; DB 2; Length 17;
Best Local Similarity 84.6%; Pred. No. 1.4e+06;
Matches 11; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 1 UGAGAGGGGCGUG 13
Db 14 TGAGAGGGGCTGG 2
RESULT 14
AX215300/c
LOCUS AX215300 17 bp RNA linear PAT 07-SEP-2001
DEFINITION Sequence 742 from Patent WO0159103.
ACCESSION AX215300
VERSION AX215300.1 GI:15525343
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1
AUTHORS Blatt,L., McSwiggen,J. and Chowrira,B.M.
TITLE Method and reagent for the modulation and diagnosis of cd20 and nogo gene expression
JOURNAL Patent: WO 0159103-A 742 16-AUG-2001;
RIBOZYME PHARMACEUTICALS, INC. (US) ; Blatt, Lawrence (US) ; McSwiggen, James (US) ; Chowrira, Bharat M. (US)
FEATURES Location/Qualifiers
source 1..17
/organism="synthetic construct"

/mol_type="unassigned RNA"
/db_xref="taxon:32630"
/note="Nucleic Acid"

ORIGIN

Query Match 54.2%; Score 13; DB 2; Length 17;
Best Local Similarity 84.6%; Pred. No. 1.4e+06;
Matches 11; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 UGAGAGGGGCGUG 13
:|||||:|
Db 13 TGAGAGGGGCTGG 1

RESULT 15

AX298773/c
LOCUS AX298773 20 bp DNA linear PAT 26-NOV-2001
DEFINITION Sequence 407 from Patent WO0183749.

ACCESSION AX298773

VERSION AX298773.1 GI:17128763

KEYWORDS

SOURCE Mus sp.

ORGANISM Mus sp.

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridea; Muridae; Murinae; Mus.

REFERENCE

AUTHORS

1 Bachmanov, A.A., Beauchamp, G.K., Chatterjee, A., de Jong, P.J., Li, S.,

Li, X., Ohmen, J.D., Reed, D.R., Ross, D. and Tordoff, M.G.

Gene and sequence variation associated with sensing carbohydrate

compounds and other sweeteners

Patent: WO 0183749-A 407 08-NOV-2001;

WARNER-LAMBERT COMPANY (US) ; The Monell Chemical Senses Center

(US)

FEATURES

source

1..20

/organism="Mus sp."

/mol_type="unassigned DNA"

/db_xref="taxon:10095"

ORIGIN

Query Match 54.2%; Score 13; DB 2; Length 20;
Best Local Similarity 84.6%; Pred. No. 1.3e+06;
Matches 11; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 UGAGAGGGGCGUG 13
:|||||:|
Db 19 TGAGAGGGGCTGG 7

Search completed: October 16, 2006, 14:52:12

Job time : 591.797 secs

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GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 16, 2006, 14:04:23 ; Search time 1032.18 Seconds
(without alignments)
1300.222 Million cell updates/sec

Title: US-10-604-726A-6034
Perfect score: 24
Sequence: 1 ugagagggcgguuagcgucc 24
Scoring table: IDENTITY NUC
Gapop 10_0 , Gapext 1.0

Searched: 48236798 seqs, 27959665780 residues

Total number of hits satisfying chosen parameters: 56556

Minimum DB seq length: 0
Maximum DB seq length: 30

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*

1: gb_est1:*
2: gb_est3:*
3: gb_est4:*
4: gb_est5:*
5: gb_est6:*
6: gb_est7:*
7: gb_est8:*
8: gb_est9:*
9: gb_est10:*
10: gb_est11:*
11: gb_est12:*
12: gb_est13:*
13: gb_est14:*
14: gb_est15:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
C 1	13.4	55.8	27	14	AJ591134	AJ591134 Arabidops
C 2	12.6	52.5	24	11	AZ806300	AZ806300 2M0068F13
C 3	12.2	50.8	28	13	CZ443094	CZ443094 IBBD03.f
C 4	12	50.0	22	1	AI473941	AI473941 tm04c11.x
C 5	12	50.0	25	10	R89803	R89803 vp91b12.r1
C 6	11.8	49.2	27	14	AG613296	AG613296 Escherich
C 7	11.8	49.2	28	14	ATH531105	ATH531105 Arabidops
C 8	11.8	49.2	29	11	AZ346559	AZ346559 1M0081M15
C 9	11.6	48.3	21	11	AZ654730	AZ654730 1M0529P05
C 10	11.6	48.3	27	11	AZ970595	AZ970595 2M0243118
C 11	11.6	48.3	27	12	CG712990	CG712990 1119029H1
C 12	11.6	48.3	27	12	CG725093	CG725093 1119083H1
C 13	11.6	48.3	30	14	AB081884	AB081884 Drosophil
C 14	11.4	47.5	25	11	AZ794596	AZ794596 2M0048M20
C 15	11.4	47.5	30	11	AZ375590	AZ375590 1M0129H06
C 16	11.2	46.7	24	11	AZ341038	AZ341038 1M0073B16
C 17	11.2	46.7	25	11	AZ820085	AZ820085 2M0092001
C 18	11.2	46.7	27	14	AJ591135	AJ591135 Arabidops
C 19	11	45.8	20	11	AZ846437	AZ846437 2M0146E10

20	11	45.8	21	11	AZ493166
C 21	11	45.8	21	11	AZ836049
22	11	45.8	25	11	AZ945526
23	11	45.8	27	11	AZ948983
24	11	45.8	28	11	AZ441037
25	11	45.8	28	11	AZ802448
C 26	11	45.8	28	12	CG725337
C 27	11	45.8	29	13	CZ443020
C 28	11	45.8	30	11	AZ976285
C 29	10.8	45.0	22	1	AI183338
C 30	10.8	45.0	27	14	TA385H06Q
C 31	10.6	44.2	20	11	AZ346729
C 32	10.6	44.2	25	11	AZ851549
C 33	10.6	44.2	26	12	AZ786348
C 34	10.6	44.2	26	12	CG729580
C 35	10.6	44.2	28	11	AZ591936
C 36	10.6	44.2	28	13	CZ472926
C 37	10.6	44.2	29	11	AZ406476
C 38	10.6	44.2	30	11	AZ460736
C 39	10.6	44.2	30	12	CG717040
C 40	10.6	44.2	30	13	CZ473194
C 41	10.4	43.3	19	11	AZ595016
C 42	10.4	43.3	22	1	AA978171
C 43	10.4	43.3	24	11	AZ786207
C 44	10.4	43.3	26	13	CW020366
C 45	10.4	43.3	28	11	AZ665590

ALIGNMENTS

RESULT 1	AJ591134/c	27 bp	DNA	linear	GSS 15-JAN-2004
LOCUS	Arabidopsis thaliana T-DNA flanking sequence, left border, clone				
DEFINITION	S80805, genomic survey sequence.				
ACCESSION	AJ591134				
VERSION	AJ591134.1	GI:37940758			
KEYWORDS	GSS; left border; T-DNA flanking sequence.				
SOURCE	Arabidopsis thaliana (thale cress)				
ORGANISM	Arabidopsis thaliana				
REFERENCE	1				
AUTHORS	Brunaud, V., Balzergue, S., Dubreucq, B., Aubourg, S., Samson, F., Chauvin, S., Bechtold, N., Cruaud, C., DeRose, R., Pelletier, G., Lepiniec, L., Caboche, M., and Lecharny, A.				
TITLE	T-DNA integration into the Arabidopsis genome depends on sequences of pre-insertion sites				
JOURNAL	EMBO Rep. 3 (12), 1152-1157 (2002)				
PUBMED	12446565				
REFERENCE	2 (bases 1 to 27)				
AUTHORS	Balzergue, S.				
TITLE	Direct Submission				
JOURNAL	Submitted (23-OCT-2003) Balzergue S., UMRGV, INRA/CNRS, 2 rue Gaston Cremieux, 91057 Evry cedex, FRANCE				
COMMENT	PCR was performed on DNA from transformants of Arabidopsis thaliana plants from INRA (Versailles). The DNA fragment(s) resulting from the PCR were directly sequenced from the left or the right border to determine the genomic sequence flanking the insertion. T-DNA derived sequences were removed. Information to order the corresponding mutant line and a link to a database providing a graphical display of the insertion site are available at http://dbgap.versailles.inra.fr/publiclines/ . This sequence has been generated in the framework of the French plant genomics program 'genoplante' (http://www.genoplante.com and http://genoplante-info.infobiogen.fr).				
FEATURES	Location/Qualifiers				
source	1..27				
	/organism="Arabidopsis thaliana"				
	/mol_type="genomic DNA"				
	/db_xref="taxon:3702"				

misc_feature 1..27 /clone="T-DNA flanking sequence /note="T-DNA insertion lines" /clone lib="Arabidopsis thaliana T-DNA insertion lines" /ecotype="Waasilewskija" /note="T-DNA flanking sequence left border"

ORIGIN

Query Match 55.8%; Score 13.4; DB 14; Length 27; Best Local Similarity 73.3%; Pred. No. 3.1e+05; Matches 11; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 5 AGGGGCGUGUUAAGG 19 |||||:|:|:| Db 21 AGGGGCTGTTAAG 7

RESULT 2

AZ806300 24 bp DNA linear GSS 20-FEB-2001 LOCUS 2M0068F13F Mouse 10kb plasmid UUGCLM library Mus musculus genomic DEFINITION clone UUGC2M0068F13 F, genomic survey sequence.

ACCESSION AZ806300 GI:12967111 VERSION AZ806300.1 KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus.

1 (bases 1 to 24)

REFERENCE 1 (bases 1 to 24) Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A., and Wright, D., Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

Unpublished (2000)

Contact: Robert B. Weiss

University of Utah Genome Center

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: dunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0068 row: F column: 13

Seq primer: CGTTGTAACGACGCGCCAGT

Class: plasmid ends

High quality sequence stop: 24.

FEATURES

source

1..24 /organism="Mus musculus" /mol_type="genomic DNA" /strain="C57BL/6J" /db_xref="taxon:10090" /clone="UUGC2M0068F13" /sex="Male" /lab_host="E. Coli strain XL10-Gold, TI-resistant, F-" /clone lib="Mouse 10kb plasmid UUGCLM library" /notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative

of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 52.5%; Score 12.6; DB 11; Length 24; Best Local Similarity 57.9%; Pred. No. 6.9e+05; Matches 11; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 1 UGAGAGGGCGUGUUAAGG 19 :|||:|:|:| Db 5 TGGGAGTGGGTAGG 23

RESULT 3

CZ443094/c

LOCUS

DEFINITION

IBB8D03.fwd HIV-vector integration sites from well-expressed proviruses in human Jurkat T cells Homo sapiens genomic clone

IBB8D03.fwd, genomic survey sequence.

ACCESSION CZ443094

VERSION CZ443094.1

KEYWORDS GSS.

SOURCE Homo sapiens (human)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 28)

REFERENCE 1 (bases 1 to 28)

AUTHORS Lewinski, M.K., Bisgrove, D., Shinn, P., Chen, H., Hoffmann, C., Hannenhalli, S., Verdin, E., Berry, C.C., Ecker, J.R. and Bushman, F.D.

Genome-wide analysis of chromosomal features repressing human immunodeficiency virus transcription

J. Virol. 79 (11), 6610-6619 (2005)

15890899

Contact: Bushman FD

Department of Microbiology

University of Pennsylvania School of Medicine

402C Johnson Pavilion, 3610 Hamilton Walk, Philadelphia, PA

19104-6076, USA

Tel: 215 573 8732

Fax: 215 573 4856

Email: bushman@mail.med.upenn.edu

Class: PCR with specific primers.

Location/Qualifiers

1..28

/organism="Homo sapiens"

/mol_type="genomic DNA"

/db_xref="taxon:9606"

/clone="IBB8D03.fwd"

/cell_line="Jurkat"

/clone lib="HIV-vector integration sites from well-expressed proviruses in human Jurkat T cells"

/note="Vector: LTR-Tat-IRES-GFP (pEV731); We have investigated regulatory sequences in noncoding human DNA that are associated with repression of an integrated human immunodeficiency virus type 1 (HIV-1) promoter. HIV-1 integration results in the formation of precise and homogeneous junctions between viral and host DNA, but integration takes place at many locations. Thus, the variation in HIV-1 gene expression at different integration sites reports the activity of regulatory sequences at nearby chromosomal positions. Negative regulation of HIV transcription is of particular interest because of its association with maintaining HIV in a latent state in cells from infected patients. To identify chromosomal regulators of HIV transcription, we infected Jurkat T cells with an HIV-based vector transducing green fluorescent protein (GFP) and separated cells into

populations containing well-expressed (GFP-positive) or poorly expressed (GFP-negative) proviruses. We then determined the chromosomal locations of the two classes by sequencing 971 junctions between viral and cellular DNA. Possible effects of endogenous cellular transcription were characterized by transcriptional profiling, low-level GFP expression correlated with integration in (i) gene deserts, (ii) centromeric heterochromatin, and (iii) very highly expressed cellular genes. These data provide a genome-wide picture of chromosomal features that repress transcription and suggest models for transcriptional latency in cells from HIV-infected patients."

ORIGIN

Query Match 50.0%; Score 12.2; DB 13; Length 28;
Best Local Similarity 64.7%; Pred. No. 1.1e+06;
Matches 11; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 3 AGAGGGGCGUUAAGC 19
|||||||:|:|
Db 20 AGAGGGGCGCTTGGG 4

RESULT 4

AI473941/c

LOCUS

DEFINITION tm04c11.x1 NCI CGAP Col4 Homo sapiens cDNA clone IMAGE:2155604 3' similar to TR:Q06459 Q06459 NUCLEOLIN.; mRNA sequence.

ACCESSION

AI473941

VERSION

AI473941.1

KEYWORDS

EST.

SOURCE

Homo sapiens (human)

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

Hominidae; Homo

1 (bases 1 to 22)

NCI-CCGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

Tumor Gene Index

Unpublished (1997)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs@mail.nih.gov

Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.

Emmert-Buck, M.D., Ph.D.

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CCGAP clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

www-bio.llnl.gov/bbrp/image/image.html

Trace considered overall poor quality

Seq primer: -40UP from Gibco

High quality sequence stop: 1.

Location/Qualifiers

1..22

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:2155604"

/tissue_type="moderately-differentiated adenocarcinoma"

/lab_host="DH10B"

/clone_lib="NCI CGAP Col4"

/note="Organ: colon; Vector: pCMV-SPORT6; Site 1: SalI;

Site 2: NotI; Cloned unidirectionally. Primer: Oligo dt.

Average insert size 1.7 Kb. Life Technologies catalog #:

11531-019"

ORIGIN

Query Match 50.0%; Score 12; DB 1; Length 22;
Best Local Similarity 70.0%; Pred. No. 1.3e+06;
Matches 14; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY

2

GAGAGGGGCGUUAAGCG 21

|||||||:|:|

Db 20 GAGAGGGGCGGTCGAGGG 1

RESULT 5

R89803/c

LOCUS

DEFINITION

YP91b12.r1 Soares fetal liver spleen INFLS Homo sapiens cDNA clone

IMAGE:194783 5' similar to gb:X63526 ELONGATION FACTOR 1-GAMMA

(HUMAN); mRNA sequence.

ACCESSION R89803

VERSION R89803.1

KEYWORDS

EST.

SOURCE

Homo sapiens (human)

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

Hominidae; Homo

1 (bases 1 to 25)

Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M.,

Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M.,

Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F.,

Trevaskis, E., Watson, R., Williamson, A., Wohlmann, P., and

Wilson, R.

The WashU-Merck EST Project

Unpublished (1995)

Contact: Wilson RK

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800

Fax: 314 286 1810

Email: est@watson.wustl.edu

Insert Size: 1193

High quality sequence starts: 1

High quality sequence stops: 1

Source: IMAGE Consortium, LLNL

This clone is available royalty-free through LLNL; contact the

IMAGE Consortium (info@image.llnl.gov) for further information.

Trace considered overall poor quality

Insert Length: 1193 Std Error: 0.00

Seq primer: M13RF1

High quality sequence stop: 1.

Location/Qualifiers

1..25

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="GDB:3763833"

/db_xref="taxon:9606"

/clone="IMAGE:194783"

/sex="male"

/dev_stage="20 week-post conception fetus"

/lab_host="DH10B (ampicillin resistant)"

/clone_lib="Soares fetal liver spleen INFLS"

/note="Organ: Liver and Spleen; Vector: pT7T3D (Pharmacia)

with a modified polylinker; Site 1: Pac I; Site 2: Eco RI;

1st strand cDNA was primed with a Pac I - oligo(dT) primer

[5' AACTGGAAGAATTAATTAAGATCTTTTTTTTTTTTTTTT 3'],

double-stranded cDNA was ligated to Eco RI adaptors

(Pharmacia), digested with Pac I and cloned into the Pac I

and Eco RI sites of the modified pT73 vector. Library

went through one round of normalization. Library

constructed by Bento Soares and M. Fatima Bonaldo."

ORIGIN

Query Match 50.0%; Score 12; DB 10; Length 25;
Best Local Similarity 75.0%; Pred. No. 1.3e+06;
Matches 9; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 6 GGGGCGUUA 17

|||||||:|:|

Db 12 GGGGCGGTAA 1

```

RESULT 6
AG613296/c
LOCUS
DEFINITION
  Escherichia coli K12 MG1655 DNA, clone: 431F, genomic survey
  sequence.
ACCESSION
  AG613296
VERSION
  AG613296.1
KEYWORDS
  GI:41224745
SOURCE
  Escherichia coli K12
ORGANISM
  Escherichia coli K12
  Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
  Enterobacteriaceae; Escherichia.
REFERENCE
  1 Hayaashi,K., Morooka,N., Mori,H. and Horiuchi,T.
  A more accurate sequence comparison between genomes of Escherichia
  coli K12 W3110 and MG1655 strains
  Unpublished
JOURNAL
  2 (bases 1 to 27)
Hayaashi,K., Morooka,N. and Horiuchi,T.
Direct Submission
TITLE
  Submitted (19-JAN-2004) Takashi Horiuchi, National Institute for
  Basic Biology, Gene Expression and Regulation II; 38 Nishigo-naka,
  Myodaiji-cho, Okazaki, Aichi 444-8595, Japan
  (E-mail:kishori@nibb.ac.jp, Tel:81-564-55-7690, Fax:81-564-55-7695)
  Location/Qualifiers
FEATURES
  source
    1..27
    /organism="Escherichia coli K12"
    /mol_type="genomic DNA"
    /strain="K12"
    /sub_strain="MG1655"
    /db_xrefs="taxon:83333"
    /clone="431F"
    /notes="The 5' end of this sequence corresponds to 9729(c)
    of Acc#: AE000431.
    This is located within REP element."
ORIGIN
  Query Match 49.2%; Score 11.8; DB 14; Length 27;
  Best Local Similarity 73.3%; Pred. No. 1.6e+06;
  Matches 11; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
QY 8 GGCUGGUUAGGCGU 22
Db 23 GGCCGGATAGGCGT 9
RESULT 7
ATH531105
LOCUS
DEFINITION
  Arabidopsis thaliana T-DNA flanking sequence, left border, clone
  225H06, genomic survey sequence.
ACCESSION
  AJ531105
VERSION
  AJ531105.1
KEYWORDS
  GI:26799365
SOURCE
  Arabidopsis thaliana
  Arabidopsis thaliana
  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
  Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
  rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE
  1 Brunaud,V., Balzergue,S., Dubreucq,B., Aubourg,S., Samson,F.,
  Chauvin,S., Bechtold,N., Cruaud,C., Dekose,R., Pelletier,G.,
  Lepiniec,L., Caboche,M. and Lecharny,A.
  T-DNA integration into the Arabidopsis genome depends on sequences
  of pre-insertion sites
  EMBO Rep. 3 (12), 1152-1157 (2002)
JOURNAL
  PUBLISHED
  12446565
AUTHORS
  Balzergue,S.
TITLE
  Direct Submission
JOURNAL
  Submitted (21-NOV-2002) Balzergue S., UMRGV, INRA/CNRS, 2 rue
  Gaston Cremieux, 91057 Evry cedex, FRANCE
  PCR was performed on DNA from transformants of Arabidopsis thaliana
  plants from INRA (Versailles). The DNA fragment(s) resulting from
  the PCR were directly sequenced from the left or the right border
  to determine the genomic sequence flanking the insertion. T-DNA
  derived sequences were removed. Information to order the
  corresponding mutant line and a link to a database providing a
  graphical display of the insertion site are available at
  http://dbgap.versailles.inra.fr/publiclines/. This sequence has
  been generated in the framework of the French plant genomics
  program 'Genoplatte' (http://www.genoplatte.com and
  http://genoplatte-info.infobiogen.fr).
  Location/Qualifiers
FEATURES
  source
    1..28
    /organism="Arabidopsis thaliana"
    /mol_type="genomic DNA"
    /cultivar="Wassilewskija"
    /db_xref="taxon:3702"
    /clone="225H06"
    /clone_lib="Arabidopsis thaliana T-DNA insertion lines"
    /ecotype="Wassilewskija"
  misc_feature
    1..28
    /note="T-DNA flanking sequence
    left border"
ORIGIN
  Query Match 49.2%; Score 11.8; DB 14; Length 28;
  Best Local Similarity 60.9%; Pred. No. 1.6e+06;
  Matches 14; Conservative 2; Mismatches 7; Indels 0; Gaps 0;
QY 2 GAGAGGGCGUGGUUAGGCGUCC 24
Db 3 GAGAGGGCGGTATATGATGTC 25
RESULT 8
AZ346559
LOCUS
DEFINITION
  1M0081M15R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
  clone UUGC1M0081M15 R, genomic survey sequence.
ACCESSION
  AZ346559
VERSION
  AZ346559.1
KEYWORDS
  GI:10425796
SOURCE
  Mus musculus (house mouse)
ORGANISM
  Mus musculus
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
  Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
  1 (bases 1 to 29)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
  Irlam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
  Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
  Niederhausern,A. and Wright,D.,Weiss,R.
  Mouse whole genome scaffolding with paired end reads from 10kb
  plasmid inserts
  Unpublished (2000)
JOURNAL
  Contact: Robert B. Weiss
COMMENT
  University of Utah Genome Center
  University of Utah
  Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
  84112, USA
  Tel: 801 585 5606
  Fax: 801 585 7177
  Email: ddunne@genetics.utah.edu
  Insert Length: 10000 Std Error: 0.00
  Plate: 0081 row: M column: 15
  Seq primer: CACACAGGAACAGCTATGACC
  Class: plasmid ends
  High quality sequence stop: 29.
  Location/Qualifiers
FEATURES
  source
    1..29
    /organism="Mus musculus"
    /mol_type="genomic DNA"

```



```

/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0529P05"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (GI|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

```

ORIGIN

```

Query Match      49.2%; Score 11.8; DB 11; Length 29;
Best Local Similarity 66.7%; Pred. No. 1.6e+06;
Matches 10; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

```

```

QY 4 GAGGGCGUGGUUAG 18
   |||||:::||||
Db 6 GAAGGTCTGGTTAAG 20

```

RESULT 9

```

AZ654730/c
LOCUS
DEFINITION
1M0529P05F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0529P05 F, genomic survey sequence.

```

```

ACCESSION
AZ654730
VERSION
AZ654730.1 GI:11791876
KEYWORDS
GSS.
SOURCE
Mus musculus (house mouse)

```

ORGANISM

```

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.

```

REFERENCE

```

AUTHORS
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.

```

```

TITLE
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

```

JOURNAL

```

COMMENT
Unpublished (2000)

```

CONTACT

```

Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA

```

```

Tel: 801 585 5606
Fax: 801 585 7177

```

```

Email: ddunn@genetics.utah.edu

```

```

Insert Length: 10000 Std Error: 0.00

```

```

Plate: 0529 row: P column: 05

```

```

Seq primer: CGTTGTAACGACGCCAGT

```

```

Class: plasmid ends

```

```

High quality sequence stop: 21.

```

FEATURES

```

Location/Qualifiers

```

```

1..21

```

```

/organism="Mus musculus"

```

FEATURES

```

Location/Qualifiers

```

```

1..27

```

source

```

/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0529P05"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (GI|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

```

ORIGIN

```

Query Match      48.3%; Score 11.6; DB 11; Length 21;
Best Local Similarity 66.7%; Pred. No. 1.9e+06;
Matches 12; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

```

```

QY 2 GAGAGGGCGUGGUUAGG 19
   |||||:::||||
Db 19 GGGTGGGATCGGTAAG 2

```

RESULT 10

AZ970595

LOCUS

```

DEFINITION
2M0243118R Mouse 10kb plasmid UUGC2M library Mus musculus genomic
clone UUGC2M0243118 R, genomic survey sequence.

```

```

ACCESSION
AZ970595
VERSION
AZ970595.1 GI:13841822
KEYWORDS
GSS.
SOURCE
Mus musculus (house mouse)

```

ORGANISM

```

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.

```

REFERENCE

```

AUTHORS
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.

```

```

TITLE
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

```

JOURNAL

```

COMMENT
Unpublished (2000)

```

CONTACT

```

Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA

```

```

Tel: 801 585 5606
Fax: 801 585 7177

```

```

Email: ddunn@genetics.utah.edu

```

```

Insert Length: 10000 Std Error: 0.00

```

```

Plate: 0243 row: I column: 18

```

```

Seq primer: CACACAGGAACAGCTATGACC

```

```

Class: plasmid ends

```

```

High quality sequence stop: 27.

```

FEATURES

```

Location/Qualifiers

```

```

1..27

```

source

```

/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0243118"
/sex="Female"
/lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC2M library"
/notes="Vector: FWD42nv; Purified genomic DNA from M. musculus C57BL/6J (female) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (G14732114|GB|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

```

ORIGIN

```

Query Match      48.3%; Score 11.6; DB 11; Length 27;
Best Local Similarity 61.1%; Pred. No. 1.9e+06;
Matches 11; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

```

```

QY      2 GAGAGGGCGUGGUUAGG 19
      |||||:::||:|
Db      1 GCGAGTGGGGGTAGGG 18

```

RESULT 11

```

CG712990/c
LOCUS      27 bp      DNA      linear      GSS 20-OCT-2003
DEFINITION 1119029H12.2EL.Y1 1119 - RescueMu Grid AA Zea mays genomic, genomic survey sequence.
ACCESSION  CG712990
VERSION     CG712990.1 GI:37738896
KEYWORDS    GSS.
SOURCE      Zea mays
ORGANISM    Zea mays

```

REFERENCE

```

AUTHORS    Walbot,V.
TITLE       Maize genomic sequences found using engineered RescueMu transposon
JOURNAL     Unpublished (2001)
COMMENT     Department of Biological Sciences
            Stanford University
            855 California Ave, Palo Alto, CA 94304, USA
            Tel: 650 723 2227
            Fax: 650 725 8221
            Email: walbot@stanford.edu
            Possible ligation site of ends cut by 2 different endonucleases.
            Reverse complemented post-ligation sequence from source sequence.
            Plate: 1119029 row: H column: 12
            Class: transposon-tagged.
            Location/Qualifiers
              1..27

```

FEATURES

source

```

/organism="Zea mays"
/mol_type="genomic DNA"
/cultivar="mixed background W23/A188/B73/K55"
/db_xref="taxon:4577"
/tissue_type="leaf"

```

```

/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="1119 - RescueMu Grid AA"
/notes="Organ: leaf; Vector: RescueMu (engineered from pBlueScript backbone); Site_1: BamHI; Site_2: BglII; RescueMu is a 4.9 kb, modified maize Mu transposon designed to allow plasmid rescue from total genomic DNA. Mu elements insert preferentially into transcription units. For more information on RescueMu, go to the web site 'www.zmdb.iastate.edu' and follow the links for 'RescueMu.' Grid AA was grown at UC San Diego in 2002. DNA was extracted from leaf strips, double digested using BamHI and BglII, and ligated to form circular plasmids. DH10B cells were transformed and then screened on LB plates with ampicillin."

```

ORIGIN

```

Query Match      48.3%; Score 11.6; DB 12; Length 27;
Best Local Similarity 61.1%; Pred. No. 1.9e+06;
Matches 11; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

```

```

QY      4 GAGGGCGUGGUUAGCGC 21
      |||||:::||:|
Db      18 GATGAGCTGTTTATGGCG 1

```

RESULT 12

```

CG725093/c
LOCUS      27 bp      DNA      linear      GSS 20-OCT-2003
DEFINITION 1119083H11.2EL.Y1 1119 - RescueMu Grid AA Zea mays genomic, genomic survey sequence.
ACCESSION  CG725093
VERSION     CG725093.1 GI:37762551
KEYWORDS    GSS.
SOURCE      Zea mays
ORGANISM    Zea mays

```

REFERENCE

```

AUTHORS    Walbot,V.
TITLE       Maize genomic sequences found using engineered RescueMu transposon
JOURNAL     Unpublished (2001)
COMMENT     Department of Biological Sciences
            Stanford University
            855 California Ave, Palo Alto, CA 94304, USA
            Tel: 650 723 2227
            Fax: 650 725 8221
            Email: walbot@stanford.edu
            Possible ligation site of ends cut by 2 different endonucleases.
            Reverse complemented post-ligation sequence from source sequence.
            Plate: 1119083 row: H column: 11
            Class: transposon-tagged.
            Location/Qualifiers
              1..27

```

FEATURES

source

```

/organism="Zea mays"
/mol_type="genomic DNA"
/cultivar="mixed background W23/A188/B73/K55"
/db_xref="taxon:4577"
/tissue_type="leaf"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="1119 - RescueMu Grid AA"
/notes="Organ: leaf; Vector: RescueMu (engineered from pBlueScript backbone); Site_1: BamHI; Site_2: BglII; RescueMu is a 4.9 kb, modified maize Mu transposon designed to allow plasmid rescue from total genomic DNA. Mu elements insert preferentially into transcription units. For more information on RescueMu, go to the web site 'www.zmdb.iastate.edu' and follow the links for 'RescueMu.' Grid AA was grown at UC San Diego in 2002. DNA was extracted from leaf strips, double digested using

```

BamHI and BglII, and ligated to form circular plasmids. DH10B cells were transformed and then screened on LB plates with ampicillin."

ORIGIN

Query Match 48.3%; Score 11.6; DB 12; Length 27;
Best Local Similarity 61.1%; Pred. No. 1.9e+06;
Matches 11; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 4 GAGGGGCGUGUUAAGCGC 21
||| | : : : : : |||

Db 18 GATGAGCTGTTATGGC 1

RESULT 13

AB081884

LOCUS

DEFINITION Drosophila melanogaster DNA, clone:1(2)SH2 0127, genomic survey

sequence.

AB081884

VERSION AB081884.1 GI:21623894

SOURCE GSS.

ORGANISM Drosophila melanogaster (fruit fly)

Neoptera; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

Ephidroidae; Drosophilidae; Drosophila.

REFERENCE 1

AUTHORS Oh, S. W., Kingsley, T., Shin, H. H., Zheng, Z., Chen, H. W., Chen, X.,

Wang, H., Ruan, P., Moody, M. and Hou, S. X.

TITLE A p-element insertion screen identified mutations in 455 novel

essential genes in Drosophila

Genetics 163 (1), 195-201 (2003)

PUBMED 12586707

REFERENCE 2 (bases 1 to 30)

AUTHORS Oh, S., Kingsley, T., Shin, H., Zheng, Z., Chen, H. and Hou, S.

TITLE Direct Submission

JOURNAL Submitted (21-MAR-2002) Suwan Oh, The Laboratory of Immunobiology,

National Institutes of Health, National Cancer Institute,

Frederick; 1050 Boyles st., Frederick, Maryland 21702-1201, USA

(E-mail: ohsuwan@mail.ncifcrf.gov, Tel:1-301-846-7314,

Fax:1-301-846-6145)

FEATURES

source

1. 30

/organism="Drosophila melanogaster"

/mol_type="genomic DNA"

/db_xref="taxon:7227"

/clone="1(2)SH2 0127"

ORIGIN

Query Match 48.3%; Score 11.6; DB 14; Length 30;
Best Local Similarity 61.1%; Pred. No. 2e+06;
Matches 11; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 6 GGGGCGUGUUAAGCGCUC 23
||| | : : : : : |||

Db 6 GGGTCTTATAAGCGCTC 23

RESULT 14

AZ794596

LOCUS

DEFINITION 2M0048M20F Mouse 10kb plasmid UUGC1M library Mus musculus genomic

clone UUGC2M0048M20 F, genomic survey sequence.

ACCESSION AZ794596

VERSION AZ794596.1 GI:12940723

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;

Sciurognathi; Murioidea; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 25)

AUTHORS

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D. Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts

Unpublished (2000)

Contact: Robert B. Weiss

University of Utah Genome Center

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0048 row: M column: 20

Seq primer: CGTTGTAAACGACGCGCCAGT

Class: plasmid ends

High quality sequence stop: 25.

FEATURES

source

1. 25

Location/Qualifiers

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUGC2M0048M20"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, TI-resistant, F-"

/clone_lib="Mouse 10kb plasmid UUGC1M library"

/note="Vector: PWD42nv; Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA

was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA

was blunt end-repaired with T4 DNA polymerase and T4

ligonucleotide kinase. Adaptor oligonucleotides were

ligated to the blunt ends in high molar excess. The

adaptor DNA was purified and size-selected for a 9.5 to

10.5 kb range using preparative agarose gel

electrophoresis. Vector DNA was prepared from a derivative

of PWD42 [GI:4732114|gb|AF129072.1], a copy-number

inducible derivative of plasmid R1. The vector was ligated

with adaptors complementary to the insert adaptors and

purified. The sheared, adaptor mouse DNA was annealed to

adaptor vector DNA, and transformed into

chemically-competent E. coli XL10-Gold (Stratagene) cells

and selected for ampicillin resistance."

ORIGIN

Query Match 47.5%; Score 11.4; DB 11; Length 25;

Best Local Similarity 57.1%; Pred. No. 2.4e+06;

Matches 12; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 1 UGAGAGGGCGUGUUAAGCGC 21
: ||||| : : : : : |||

Db 5 TGGGAGGGCGGTGTGAGGGG 25

RESULT 15

AZ375590/c

LOCUS

DEFINITION 1M0129H06F Mouse 10kb plasmid UUGC1M library Mus musculus genomic

clone UUGC1M0129H06 F, genomic survey sequence.

ACCESSION AZ375590

VERSION AZ375590.1 GI:10489290

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;

Sciurognathi; Muroidae; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 30)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb
JOURNAL plasmid inserts
COMMENT Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0129 row: H column: 06
Seq primer: CGTTGTAAACGACGCGCAGT
Class: plasmid ends
High quality sequence stop: 30.
FEATURES
source
1..30
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0129H06"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

ORIGIN
Query Match 47.5%; Score 11.4; DB 11; Length 30;
Best Local Similarity 52.4%; Pred. No. 2.4e+06;
Matches 11; Conservative 4; Mismatches 6; Indels 0; Gaps 0;
QY 1 UGAGAGGGCGGCUUUAAGCGG 21
:|||||:|:|:|:|
DB 27 TGAAGAGGAGTTGTTAAGGGG 7

Search completed: October 16, 2006, 15:51:23
Job time : 1034.18 secs

GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 16, 2006, 14:11:03 ; Search time 55.5789 Seconds
(without alignments)
807.979 Million cell updates/sec

Title: US-10-604-726A-6034

Perfect score: 24

Sequence: 1 ugagagggcgguuagggcucc 24

Scoring table: IDENTITY NUC

Gapop 10_0 , Gapext 1.0

Searched: 1403666 seqs, 935554401 residues

Total number of hits satisfying chosen parameters: 1097684

Minimum DB seq length: 0
Maximum DB seq length: 30

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents NA: *
1: /EMC_Celerra_SID33/ptodata/2/ina/1 COMB.seq: *
2: /EMC_Celerra_SID33/ptodata/2/ina/5 COMB.seq: *
3: /EMC_Celerra_SID33/ptodata/2/ina/6A COMB.seq: *
4: /EMC_Celerra_SID33/ptodata/2/ina/6B COMB.seq: *
5: /EMC_Celerra_SID33/ptodata/2/ina/7 COMB.seq: *
6: /EMC_Celerra_SID33/ptodata/2/ina/8 COMB.seq: *
7: /EMC_Celerra_SID33/ptodata/2/ina/9 COMB.seq: *
8: /EMC_Celerra_SID33/ptodata/2/ina/PP COMB.seq: *
9: /EMC_Celerra_SID33/ptodata/2/ina/RE COMB.seq: *
10: /EMC_Celerra_SID33/ptodata/2/ina/backfiles1.seq: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	15.2	63.3	28	3	US-08-814-052-53
C 2	14	58.3	25	3	US-09-396-1960-15707
C 3	13.8	57.5	22	2	US-08-179-738-12
C 4	13.8	57.5	22	2	US-08-828-145-12
C 5	13.2	55.0	25	2	US-08-295-814E-23
C 6	13.2	55.0	25	3	US-09-343-361-23
C 7	13	54.2	27	4	US-09-598-982C-7
C 8	12.8	53.3	19	2	US-08-460-751-27
C 9	12.8	53.3	25	3	US-09-641-259B-31
C 10	12.6	52.5	19	3	US-10-059-579A-123
C 11	12.6	52.5	20	3	US-09-166-186-119
C 12	12.6	52.5	20	3	US-09-313-932-119
C 13	12.6	52.5	20	3	US-09-580-052-51
C 14	12.6	52.5	21	3	US-08-520-373D-31
C 15	12.6	52.5	25	3	US-09-443-067-45
C 16	12.6	52.5	25	3	US-09-396-1960-3644
C 17	12.6	52.5	25	3	US-09-396-1960-29254
C 18	12.6	52.5	28	3	US-09-529-239D-21
C 19	12.6	52.5	30	3	US-08-940-316-65
C 20	12.6	52.5	30	3	US-08-840-316-102
C 21	12.6	52.5	30	3	US-08-809-523-65
C 22	12.6	52.5	30	3	US-08-809-523-102
C 23	12.6	52.5	30	3	US-08-471-971-65

C 24	12.6	52.5	30	3	US-08-471-971-102	Sequence 102, Appl
C 25	12.6	52.5	30	3	US-09-402-776-65	Sequence 65, Appl
C 26	12.6	52.5	30	3	US-09-402-776-102	Sequence 102, Appl
C 27	12.6	52.5	30	3	US-09-291-129-10	Sequence 10, Appl
C 28	12.6	52.5	30	3	US-08-470-246-65	Sequence 65, Appl
C 29	12.6	52.5	30	3	US-08-470-246-102	Sequence 102, Appl
C 30	12.6	52.5	30	3	US-08-316-765-65	Sequence 65, Appl
C 31	12.6	52.5	30	3	US-08-316-765-102	Sequence 102, Appl
C 32	12.6	52.5	30	3	US-09-724-475-102	Sequence 65, Appl
C 33	12.6	52.5	30	3	US-09-724-475-102	Sequence 102, Appl
C 34	12.6	52.5	30	7	PCT-US93-08849A-65	Sequence 65, Appl
C 35	12.6	52.5	30	7	PCT-US93-08849A-65	Sequence 65, Appl
C 36	12.4	51.7	24	3	US-09-630-377-11	Sequence 11, Appl
C 37	12.4	51.7	25	3	US-09-396-196G-41852	Sequence 41852, A
C 38	12.4	51.7	25	3	US-09-396-196G-58488	Sequence 58488, A
C 39	12.4	51.7	25	3	US-09-396-196G-73489	Sequence 73489, A
C 40	12.4	51.7	25	3	US-09-396-196G-78586	Sequence 78586, A
C 41	12.4	51.7	25	3	US-09-396-196G-122139	Sequence 122139, A
C 42	12.4	51.7	25	3	US-09-396-196G-122140	Sequence 122140, A
C 43	12.2	50.8	19	3	US-09-422-978-9132	Sequence 9132, Ap
C 44	12.2	50.8	20	2	US-08-117-952-440	Sequence 440, Appl
C 45	12.2	50.8	20	3	US-09-526-193A-6	Sequence 6, Appli

ALIGNMENTS

RESULT 1
US-08-814-052-53/c
; Sequence 53, Application US/08814052
; Patent No. 6015783
; GENERAL INFORMATION:
; APPLICANT: von der Osten, Claus
; APPLICANT: Cherry, Joel R.
; APPLICANT: Bjornvad, Mads E.
; APPLICANT: Vind, Jesper
; APPLICANT: Rasmussen, Michael Dolberg
; TITLE OF INVENTION: PROCESS FOR REMOVAL OR BLEACHING OF SOILING
; NUMBER OF SEQUENCES: 55
; CORRESPONDENCE ADDRESS:
; ADDRESSER: No. 60157830 No. 6015783disk of No. 6015783th America, Inc.
; STREET: 405 Lexington Avenue, Suite 6400
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10174-6401
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/814,052
; FILING DATE: 06-MAR-1997
; CLASSIFICATION: 510
; ATTORNEY/AGENT INFORMATION:
; NAME: Lambiris, Elias J
; REGISTRATION NUMBER: 33,728
; REFERENCE/DOCKET NUMBER: 4684.204-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-867-0123
; TELEFAX: 212-878-9655
; TELEX:
; INFORMATION FOR SEQ ID NO: 53:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 28 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-814-052-53

Query Match 63.3%; Score 15.2; DB 3; Length 28;

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Best Local Similarity 75.0%; Pred. No. 5.5e+02;
Matches 15; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 2 GAGAGGGGCGUGUUAAGGCG 21
Db 20 GCGAGTGGCTGGTCAAGGCG 1

RESULT 2
US-09-396-196G-15707/c
; Sequence 15707, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15707
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-396-196G-15707

Query Match 58.3%; Score 14; DB 3; Length 25;
Best Local Similarity 54.5%; Pred. No. 2e+03;
Matches 12; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 1 UGAGAGGGGCGUGUUAAGGCG 22
Db 22 TGAGATGAGCTGCTTAAAGGAT 1

RESULT 3
US-08-179-738-12/c
; Sequence 12, Application US/08179738
; Patent No. 5578462
; GENERAL INFORMATION:
; APPLICANT: Seizinger, Bernd R.
; APPLICANT: Kley, Nikolai A.
; APPLICANT: Bianchi, Albert B.
; TITLE OF INVENTION: No. 5578462el NF2 Isoforms
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Reed & Robins
; STREET: 635 Bryant Street
; CITY: Palo Alto
; STATE: California
; COUNTRY: U.S.A
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/179,738
; FILING DATE: 10-JAN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Robins, Roberta L.
; REGISTRATION NUMBER: 33,208
; REFERENCE/DOCKET NUMBER: 5998-0017
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 617-8999
; TELEFAX: (415) 327-3231
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 22 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
US-08-179-738-12

Query Match 57.5%; Score 13.8; DB 2; Length 22;
Best Local Similarity 70.6%; Pred. No. 2.5e+03;
Matches 12; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 3 AGAGGGGCGUGUUAAGG 19
Db 17 AGAGGAGCTGGTTCAGG 1

RESULT 4
US-08-628-145-12/c
; Sequence 12, Application US/08628145
; Patent No. 5872214
; GENERAL INFORMATION:
; APPLICANT: Seizinger, Bernd R.
; APPLICANT: Kley, Nikolai A.
; APPLICANT: Bianchi, Albert B.
; TITLE OF INVENTION: No. 5872214el NF2 Isoforms
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Reed & Robins
; STREET: 635 Bryant Street
; CITY: Palo Alto
; STATE: California
; COUNTRY: U.S.A
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/628,145
; FILING DATE: 04-APR-1996
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/179,738
; FILING DATE: 10-JAN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Robins, Roberta L.
; REGISTRATION NUMBER: 33,208
; REFERENCE/DOCKET NUMBER: 5998-0017
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 617-8999
; TELEFAX: (415) 327-3231
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 22 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
US-08-628-145-12

Query Match 57.5%; Score 13.8; DB 2; Length 22;
Best Local Similarity 70.6%; Pred. No. 2.5e+03;
Matches 12; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 3 AGAGGGGCGUGUUAAGG 19
Db 17 AGAGGAGCTGGTTCAGG 1

RESULT 5
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US-08-295-814E-23/c
; Sequence 23, Application US/08295814E
; Patent No. 5658786
; GENERAL INFORMATION:
; APPLICANT: Smith, Kelli E.
; APPLICANT: Borden, Laurence A.
; APPLICANT: Hartig, Paul R.
; APPLICANT: Weinschank, Richard L.
; TITLE OF INVENTION: DNA ENCODING TAURINE AND GABA
; TITLE OF INVENTION: TRANSPORTERS AND USES THEREOF
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/295,814E
; FILING DATE: DECEMBER 19, 1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 40558-B-PCT-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-278-0400
; TELEFAX: 212-391-0525
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-295-814E-23

Query Match 55.0%; Score 13.2; DB 2; Length 25;
Best Local Similarity 66.7%; Pred. No. 4.9e+03;
Matches 12; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
QY 5 AGGGCGUGGUUAGGCGU 22
Db 23 AGGTGCTGTGAAGGCAT 6

RESULT 6
US-09-343-361-23/c
; Sequence 23, Application US/09343361
; Patent No. 6225115
; GENERAL INFORMATION:
; APPLICANT: Smith, Kelli E. et al
; TITLE OF INVENTION: DNA Encoding Taurine and GABA Transporters and Uses
; TITLE OF INVENTION: Thereof
; FILE REFERENCE: 40558-D
; CURRENT APPLICATION NUMBER: US/09/343,361
; CURRENT FILING DATE: 1999-06-30
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.0 - beta
; SEQ ID NO 23
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: primer
US-09-343-361-23

Query Match 55.0%; Score 13.2; DB 3; Length 25;
Best Local Similarity 66.7%; Pred. No. 4.9e+03;
Matches 12; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
QY 5 AGGGCGUGGUUAGGCGU 22
Db 23 AGGTGCTGTGAAGGCAT 6

RESULT 7
US-09-598-982C-7
; Sequence 7, Application US/09598982C
; Patent No. 6938260
; GENERAL INFORMATION:
; APPLICANT: Niles, Andrew
; APPLICANT: Haak-Frendscho, Mary
; TITLE OF INVENTION: RECOMBINANT PROTEOLYTIC TRYPTASES, ACTIVE SITE MUTANTS THEREOF,
; TITLE OF INVENTION: AND METHODS OF MAKING SAME
; FILE REFERENCE: 34506.104
; CURRENT APPLICATION NUMBER: US/09/598,982C
; CURRENT FILING DATE: 2000-06-21
; PRIOR APPLICATION NUMBER: 09/079,970
; PRIOR FILING DATE: 1998-04-15
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 7
; LENGTH: 27
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Mutagenesis oligonucleotide
US-09-598-982C-7

Query Match 54.2%; Score 13; DB 4; Length 27;
Best Local Similarity 66.7%; Pred. No. 6.2e+03;
Matches 14; Conservative 2; Mismatches 5; Indels 0; Gaps 0;
QY 4 GAGGGCGUGGUUAGGCGUCC 24
Db 1 GAGGAGCCGCTGAAGGTCTCC 21

RESULT 8
US-08-460-751-27
; Sequence 27, Application US/08460751
; Patent No. 5891628
; GENERAL INFORMATION:
; APPLICANT: Reeders, Stephen
; APPLICANT: Schneider, Michael
; APPLICANT: Glucksman, Sandra
; TITLE OF INVENTION: IDENTIFICATION OF POLYCYSTIC KIDNEY
; TITLE OF INVENTION: DISEASE GENE, DIAGNOSTICS AND TREATMENT
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/460,751
; FILING DATE: 02-JUN-1995
; CLASSIFICATION: 435
; OTHER INFORMATION: Description of Artificial Sequence: primer
; APPLICATION NUMBER: US 08/413,580
; FILING DATE: 03-MAR-1995

```
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7638-005
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-8864/9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 19 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; US-08-460-751-27

Query Match 53.3%; Score 12.8; DB 2; Length 19;
Best Local Similarity 62.5%; Pred. No. 7.3e+03;
Matches 10; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 9 GCUGGUUAGGCGUCC 24
Db 1 GCTCTTTAAGCGCTCC 16
||: :|||||:|

RESULT 9
US-09-641-2598-31/c
; Sequence 31, Application US/09641259B
; Patent No. 6468756
; GENERAL INFORMATION:
; APPLICANT: Bonini, James A
; APPLICANT: Borowsky, Beth E
; APPLICANT: Acham, Nika
; APPLICANT: Boyle, No. 64687561
; APPLICANT: Thompson, Thelma O.
; TITLE OF INVENTION: DNA Encoding SNORF25 Receptor
; FILE REFERENCE: 1795/56095-B/JPM/ADM
; CURRENT APPLICATION NUMBER: US/09/641,259B
; CURRENT FILING DATE: 2002-03-12
; PRIOR APPLICATION NUMBER: PCT/US00/04413
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 09/387,699
; PRIOR FILING DATE: 1999-08-13
; PRIOR APPLICATION NUMBER: US 09/255,376
; PRIOR FILING DATE: 1999-02-22
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 31
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primer/ Probe
; US-09-641-2598-31

Query Match 53.3%; Score 12.8; DB 3; Length 25;
Best Local Similarity 68.8%; Pred. No. 7.6e+03;
Matches 11; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 4 GAGGGGCGUGGUUAGG 19
Db 20 GAGGGGCTGCTTAATG 5
|||||:|:|:|

RESULT 10
US-10-059-579A-123/c
; Sequence 123, Application US/10059579A
; Patent No. 6835541
; GENERAL INFORMATION:
; APPLICANT: THE JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE
; APPLICANT: SUKUMAR, Saraswati
; APPLICANT: EVRON, Ella

; APPLICANT: DOOLEY, William C.
; APPLICANT: DAVIDSON, Nancy
; APPLICANT: FACKLER, Mary Jo.
; TITLE OF INVENTION: ABERRANTLY METHYLATED GENES AS MARKERS OF BREAST MALIGNANCY
; FILE REFERENCE: JHU1630-1
; CURRENT APPLICATION NUMBER: US/10/059,579A
; CURRENT FILING DATE: 2002-01-28
; PRIOR APPLICATION NUMBER: US 09/771,357
; PRIOR FILING DATE: 2001-01-26
; NUMBER OF SEQ ID NOS: 136
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 123
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: PCR antisense primer
; US-10-059-579A-123

Query Match 52.5%; Score 12.6; DB 3; Length 19;
Best Local Similarity 57.9%; Pred. No. 9.1e+03;
Matches 11; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 4 GAGGGGCGUGGUUAGGCGU 22
Db 19 GAAGGGGTAGTTAAGGGGT 1
|||||:|:|:|

RESULT 11
US-09-166-186-119/c
; Sequence 119, Application US/09166186A
; Patent No. 6080580
; GENERAL INFORMATION:
; APPLICANT: Baker, Brenda
; APPLICANT: Bennett, C. Frank
; APPLICANT: Butler, Madeline M.
; APPLICANT: Shanahan, William R.
; TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDE MODULATION OF TNF-a EXPRESSION
; FILE REFERENCE: ISPH-0322
; CURRENT APPLICATION NUMBER: US/09/166,186A
; CURRENT FILING DATE: 1998-10-05
; NUMBER OF SEQ ID NOS: 250
; SEQ ID NO 119
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: antisense sequence
; US-09-166-186-119

Query Match 52.5%; Score 12.6; DB 3; Length 20;
Best Local Similarity 63.2%; Pred. No. 9.1e+03;
Matches 12; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 4 GAGGGGCGUGGUUAGGCGU 22
Db 20 GGGGGCGGGTTGAGGGGT 2
|||||:|:|:|

RESULT 12
US-09-313-932-119/c
; Sequence 119, Application US/09313932A
; Patent No. 6228642
; GENERAL INFORMATION:
; APPLICANT: Baker, Brenda
; APPLICANT: Bennett, C. Frank
; APPLICANT: Butler, Madeline M.
; APPLICANT: Shanahan, William R.
; TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDE MODULATION OF TNF-
; TITLE OF INVENTION: EXPRESSION
; FILE REFERENCE: ISPH-0356
; CURRENT APPLICATION NUMBER: US/09/313,932A
; CURRENT FILING DATE: 1999-05-18
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; NUMBER OF SEQ ID NOS: 501
; SEQ ID NO 119
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-09-313-932-119

Query Match          52.5%; Score 12.6; DB 3; Length 20;
Best Local Similarity 63.2%; Pred. No. 9.1e+03;
Matches 12; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 4 GAGGGCGGCGUUAAGGCG 22
   |||||:|:|:|:|:|:|
Db 20 GGGGGCGGCGTGAAGGCGT 2

RESULT 13
US-09-980-052-51
; Sequence 51, Application US/09980052
; Patent No. 6670130
; GENERAL INFORMATION:
; APPLICANT: KIM, Jeong Joon; SJ HIGHTECH Co., Ltd.
; APPLICANT: KIM, Cheol Min
; APPLICANT: PARK, Hee Kyung
; TITLE OF INVENTION: Oligonucleotide for detection and identification of Mycobacterium
; FILE REFERENCE: PP05020/PCT
; CURRENT APPLICATION NUMBER: US/09/980,052
; CURRENT FILING DATE: 2001-11-28
; PRIOR APPLICATION NUMBER: KR 10-1999-0019631
; PRIOR FILING DATE: 1999-05-29
; PRIOR APPLICATION NUMBER: KR 10-1999-0019632
; PRIOR FILING DATE: 1999-05-29
; PRIOR APPLICATION NUMBER: KR 10-1999-0019633
; PRIOR FILING DATE: 1999-05-29
; PRIOR APPLICATION NUMBER: KR 10-1999-0019634
; PRIOR FILING DATE: 1999-05-29
; PRIOR APPLICATION NUMBER: KR 10-1999-0019635
; PRIOR FILING DATE: 1999-05-29
; PRIOR APPLICATION NUMBER: KR 10-2000-0018189
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 243
; SOFTWARE: KopatentIn 1.71
; SEQ ID NO 51
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: sequence of probe or primer for detecting Mycobacterium abscessus
US-09-980-052-51

Query Match          52.5%; Score 12.6; DB 3; Length 20;
Best Local Similarity 63.2%; Pred. No. 9.1e+03;
Matches 12; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 2 GAGGGCGGCGUUAAGGCG 20
   |||||:|:|:|:|:|:|
Db 1 GAGTGGGCGTGGTTTTCG 19

RESULT 14
US-08-520-373D-31/c
; Sequence 31, Application US/08520373D
; Patent No. 6451763
; GENERAL INFORMATION:
; APPLICANT: Tombran-Tink, Joyce
; APPLICANT: Steele, Fintan R
; APPLICANT: Chader, Gerald J
; APPLICANT: Becerra, Sofia P
; APPLICANT: Johnson, Lincoln V
; APPLICANT: Rodriguez, Ignacio R
; TITLE OF INVENTION: RETINAL PIGMENTED EPITHELIUM DERIVED NEUROTROPIC FACTOR
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; FILE REFERENCE: 2026-4203US1
; CURRENT APPLICATION NUMBER: US/08/520,373D
; CURRENT FILING DATE: 1995-08-29
; PRIOR APPLICATION NUMBER: 08/377,710
; PRIOR FILING DATE: 1995-01-25
; PRIOR APPLICATION NUMBER: 08/279,979
; PRIOR FILING DATE: 1994-07-25
; PRIOR APPLICATION NUMBER: 07/894,215
; PRIOR FILING DATE: 1992-06-04
; PRIOR APPLICATION NUMBER: 07/952,796
; PRIOR FILING DATE: 1992-09-24
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 31
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: SYNTHETIC
; OTHER INFORMATION: PRIMER
; OTHER INFORMATION: PRIMER 1
US-08-520-373D-31

Query Match          52.5%; Score 12.6; DB 3; Length 21;
Best Local Similarity 63.2%; Pred. No. 9.2e+03;
Matches 12; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 3 AGAGGGCGGCGUUAAGGCG 21
   |||||:|:|:|:|:|:|
Db 19 ATAAAGGCTGGTTAGGTG 1

RESULT 15
US-09-443-067-45
; Sequence 45, Application US/09443067
; Patent No. 6627794
; GENERAL INFORMATION:
; APPLICANT: COMMONWEALTH SCIENTIFIC AND INDUSTRIAL RESEARCH
; APPLICANT: ORGANISATION
; TITLE OF INVENTION: Polyphenol oxidase genes from banana, lettuce, tobacco and
; TITLE OF INVENTION: pineapple
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/443,067
; CURRENT FILING DATE: 1999-11-18
; EARLIER APPLICATION NUMBER: US 08/976,222
; EARLIER FILING DATE: 1997-11-21
; EARLIER APPLICATION NUMBER: PCT/AU98/00362
; EARLIER FILING DATE: 1998-05-19
; EARLIER APPLICATION NUMBER: AU PP3898
; EARLIER FILING DATE: 1995-05-23
; EARLIER APPLICATION NUMBER: AU PP6849
; EARLIER FILING DATE: 1997-05-19
; EARLIER APPLICATION NUMBER: AU PP5600
; EARLIER FILING DATE: 1995-09-26
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 45
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: primer
US-09-443-067-45

Query Match          52.5%; Score 12.6; DB 3; Length 25;
Best Local Similarity 63.2%; Pred. No. 9.5e+03;
Matches 12; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 5 AGGGCGGCGUUAAGGCGUC 23
   |||||:|:|:|:|:|:|
Db 6 ATGGGATGGTGAAGGTGTC 24
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Search completed: October 16, 2006, 14:47:12
Job time : 56.5789 secs

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OM nucleic - nucleic search, using sw model

Run on: October 16, 2006, 14:16:09 ; Search time 337.985 Seconds
(without alignments)
872.534 Million cell updates/sec

Title: US-10-604-726A-6034

Perfect score: 24

Sequence: 1 ugagagggcugguuagggcucc 24

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 18992170 seqs, 6143817638 residues

Total number of hits satisfying chosen parameters: 23237482

Minimum DB seq length: 0

Maximum DB seq length: 30

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications NA Main:*

- 1: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US07_PUBCOMB.seq.*
- 2: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US08_PUBCOMB.seq.*
- 3: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09A_PUBCOMB.seq.*
- 4: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09B_PUBCOMB.seq.*
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- 8: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10C_PUBCOMB.seq.*
- 9: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10D_PUBCOMB.seq.*
- 10: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10E_PUBCOMB.seq.*
- 11: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10F_PUBCOMB.seq.*
- 12: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10G_PUBCOMB.seq.*
- 13: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11A_PUBCOMB.seq.*
- 14: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11B_PUBCOMB.seq.*
- 15: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11C_PUBCOMB.seq.*
- 16: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11D_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	16.6	69.2	25	13	US-11-036-317-713202
C 2	16.2	67.5	25	9	US-10-719-900-888593
C 3	15.8	65.8	24	3	US-09-940-185-365
C 4	15.8	65.8	25	3	US-09-940-185-4341
C 5	15.8	65.8	25	13	US-11-036-317-751276
C 6	15.6	65.0	25	13	US-11-036-317-508584
C 7	15.6	65.0	25	13	US-11-036-317-648052
C 8	15.2	63.3	21	11	US-10-310-914A-310484
C 9	15.2	63.3	21	11	US-10-310-914A-310485
C 10	15.2	63.3	21	11	US-10-310-914A-310486
C 11	15.2	63.3	21	11	US-10-310-914A-310487
C 12	15.2	63.3	21	11	US-10-310-914A-594029
C 13	15.2	63.3	21	11	US-10-310-914A-1286104
C 14	15.2	63.3	22	11	US-10-310-914A-1056699
C 15	15.2	63.3	24	11	US-10-310-914A-594065
C 16	15.2	63.3	24	11	US-10-310-914A-1286102
C 17	15.2	63.3	25	9	US-10-719-900-62329

18	15.2	63.3	25	15	US-11-121-849-463132	Sequence 463132,
C 19	15	62.5	25	9	US-10-719-900-470368	Sequence 470368,
C 20	15	62.5	25	9	US-10-719-900-473457	Sequence 473457,
C 21	15	62.5	25	13	US-11-036-317-537085	Sequence 537085,
C 22	15	62.5	25	13	US-11-036-317-557262	Sequence 557262,
C 23	15	62.5	25	13	US-11-036-317-713203	Sequence 713203,
C 24	15	62.5	25	13	US-11-036-317-798014	Sequence 798014,
C 25	14.8	61.7	21	11	US-10-310-914A-752575	Sequence 752575,
C 26	14.8	61.7	21	11	US-10-310-914A-371120	Sequence 371120,
C 27	14.6	60.8	21	11	US-10-310-914A-707100	Sequence 707100,
C 28	14.6	60.8	23	11	US-10-310-914A-1006052	Sequence 1006052,
C 29	14.6	60.8	23	11	US-10-469-866-23	Sequence 23, Appli
C 30	14.6	60.8	24	9	US-10-310-914A-224322	Sequence 224322,
C 31	14.6	60.8	24	11	US-10-719-956-115627	Sequence 115627,
C 32	14.6	60.8	25	8	US-10-719-956-115627	Sequence 115627,
C 33	14.6	60.8	25	9	US-10-719-956-115627	Sequence 115627,
C 34	14.6	60.8	25	9	US-10-719-900-888594	Sequence 888594,
C 35	14.6	60.8	25	13	US-11-036-317-892224	Sequence 892224,
C 36	14.6	60.8	25	13	US-11-036-317-966783	Sequence 966783,
C 37	14.6	60.8	25	15	US-11-121-849-363	Sequence 363, App
C 38	14.6	60.8	26	11	US-10-310-914A-1006049	Sequence 1006049,
C 39	14.6	60.8	27	11	US-10-310-914A-224323	Sequence 224323,
C 40	14.4	60.0	21	12	US-10-504-589A-7	Sequence 7, Appli
C 41	14.4	60.0	24	11	US-10-310-914A-1339473	Sequence 1339473,
C 42	14.4	60.0	25	8	US-10-719-956-605791	Sequence 605791,
C 43	14.4	60.0	25	8	US-10-719-956-605792	Sequence 605792,
C 44	14.4	60.0	25	13	US-11-036-317-213436	Sequence 213436,
C 45	14.4	60.0	25	13	US-11-036-317-884459	Sequence 884459,

ALIGNMENTS

RESULT 1

US-11-036-317-713202/c
; Sequence 713202, Application US/11036317
; Publication NO. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 713202
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-713202

Query Match 69.2%; Score 16.6; DB 13; Length 25;
Best Local Similarity 65.2%; Pred. No. 8.8e+02;
Matches 15; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 2 GAGAGGGGUGGUUAGGGUCC 24

DB 24 GAGAGGGCCTGGTTCAGGAGTCC 2

RESULT 2

US-10-719-900-888593/c
; Sequence 888593, Application US/10719900
; Publication NO. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20

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; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002.11.20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 888593
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-888593

Query Match      67.5%; Score 16.2; DB 9; Length 25;
Best Local Similarity 66.7%; Pred. No. 1.4e+03;
Matches 14; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 4 GAGGGGCGUGUUAAGCGGUCC 24
Db 23 GAAGGGCTAGTTAAGGCTCC 3

RESULT 3
US-09-940-185-365
; Sequence 365, Application US/09940185
; Publication No. US20030096239A1
; GENERAL INFORMATION:
; APPLICANT: Gunderson, Kevin
; APPLICANT: Chee, Mark
; TITLE OF INVENTION: Probes and Decoder Oligonucleotides
; FILE REFERENCE: A-69605-1
; CURRENT APPLICATION NUMBER: US/09/940,185
; CURRENT FILING DATE: 2001-08-27
; PRIOR APPLICATION NUMBER: US 60/227,948
; PRIOR FILING DATE: 2000-08-25
; PRIOR APPLICATION NUMBER: US 60/228,854
; PRIOR FILING DATE: 2000-08-29
; NUMBER OF SEQ ID NOS: 4768
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 365
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Computer Generated Probe Sequence.
US-09-940-185-365

Query Match      65.8%; Score 15.8; DB 3; Length 24;
Best Local Similarity 73.7%; Pred. No. 2.1e+03;
Matches 14; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 2 GAGAGGGCGUGUUAAGGC 20
Db 4 GAGAGGCGTTGGTTAAGGC 22

RESULT 4
US-09-940-185-4341
; Sequence 4341, Application US/09940185
; Publication No. US20030096239A1
; GENERAL INFORMATION:
; APPLICANT: Gunderson, Kevin
; APPLICANT: Chee, Mark
; TITLE OF INVENTION: Probes and Decoder Oligonucleotides
; FILE REFERENCE: A-69605-1
; CURRENT APPLICATION NUMBER: US/09/940,185
; CURRENT FILING DATE: 2001-08-27
; PRIOR APPLICATION NUMBER: US 60/227,948
; PRIOR FILING DATE: 2000-08-25
; PRIOR APPLICATION NUMBER: US 60/228,854
; PRIOR FILING DATE: 2000-08-29
; NUMBER OF SEQ ID NOS: 4768
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4341
; LENGTH: 25
; TYPE: DNA

; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Computer Generated Probe Sequence.
US-09-940-185-4341

Query Match      65.8%; Score 15.8; DB 3; Length 25;
Best Local Similarity 73.7%; Pred. No. 2.1e+03;
Matches 14; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 2 GAGAGGGCGUGUUAAGGC 20
Db 5 GAGAGGCGTTGGTTAAGGC 23

RESULT 5
US-11-036-317-751276/c
; Sequence 751276, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 751276
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-751276

Query Match      65.8%; Score 15.8; DB 13; Length 25;
Best Local Similarity 68.4%; Pred. No. 2.1e+03;
Matches 13; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 UCAGAGGGCGUGUUAAGG 19
Db 25 TCAAAGGGGCGTGGTTAAGG 7

RESULT 6
US-11-036-317-508584/c
; Sequence 508584, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 508584
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-508584

Query Match      65.0%; Score 15.6; DB 13; Length 25;
Best Local Similarity 63.6%; Pred. No. 2.6e+03;
Matches 14; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 3 AGAGGGCGUGUUAAGCGUCC 24
Db 25 AGAGGCCCTGGTTACGAGGTCC 4
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RESULT 7
US-11-036-317-648052/c
; Sequence 648052, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 648052
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-648052

Query Match      65.0%; Score 15.6; DB 13; Length 25;
Best Local Similarity 63.8%; Pred. No. 2.6e+03;
Matches 14; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY      2  GAGAGGGGCGUGUUAAGGCGUC 23
Db      22 GAGAGGCCCTGGTTCAGGATC 1

RESULT 8
US-10-310-914A-310484/c
; Sequence 310484, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 310484
; LENGTH: 21
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-310484

Query Match      63.3%; Score 15.2; DB 11; Length 21;
Best Local Similarity 75.0%; Pred. No. 4.1e+03;
Matches 15; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY      1  UGAGAGGGGCGUGUUAAGGC 20
Db      21 TGAGAGGGGAGGCTAAGGC 2

RESULT 9
US-10-310-914A-310485/c
; Sequence 310485, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
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; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 310485
; LENGTH: 21
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-310485

Query Match      63.3%; Score 15.2; DB 11; Length 21;
Best Local Similarity 75.0%; Pred. No. 4.1e+03;
Matches 15; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY      1  UGAGAGGGGCGUGUUAAGGC 20
Db      21 TGAGAGGGGAGGCTAAGGC 2

RESULT 10
US-10-310-914A-310486/c
; Sequence 310486, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 310486
; LENGTH: 21
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-310486

Query Match      63.3%; Score 15.2; DB 11; Length 21;
Best Local Similarity 75.0%; Pred. No. 4.1e+03;
Matches 15; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY      1  UGAGAGGGGCGUGUUAAGGC 20
Db      21 TGAGAGGGGAGGCTAAGGC 2

RESULT 11
US-10-310-914A-310487/c
; Sequence 310487, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 310487
; LENGTH: 21
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-310487

Query Match      63.3%; Score 15.2; DB 11; Length 21;
Best Local Similarity 75.0%; Pred. No. 4.1e+03;
Matches 15; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY      1  UGAGAGGGGCGUGUUAAGGC 20
Db      21 TGAGAGGGGAGGCTAAGGC 2
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; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 310485
; LENGTH: 21
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-310485

Query Match      63.3%; Score 15.2; DB 11; Length 21;
Best Local Similarity 75.0%; Pred. No. 4.1e+03;
Matches 15; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY      1  UGAGAGGGGCGUGUUAAGGC 20
Db      21 TGAGAGGGGAGGCTAAGGC 2
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RESULT 12
US-10-310-914A-594029
; Sequence 594029, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 594029
; LENGTH: 21
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-594029

Query Match          63.3%; Score 15.2; DB 11; Length 21;
Best Local Similarity 85.0%; Pred. No. 4.1e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      2 GAGAGGGGCGUGUUAAGGCG 21
        ||||| ||||| ||||| |||||
Db      2 GAGAGGGGCGUGUUGGGGUG 21

RESULT 13
US-10-310-914A-1286104/c
; Sequence 1286104, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1286104
; LENGTH: 21
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-1286104

Query Match          63.3%; Score 15.2; DB 11; Length 21;
Best Local Similarity 85.0%; Pred. No. 4.1e+03;
Matches 16; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY      2 GAGAGGGGCGUGUUAAGGCG 21
        ||||| ||||| ||||| |||||
Db      2 GAGAGGGGCGUGUUGGGGUG 21

RESULT 14
US-10-310-914A-1056699/c
; Sequence 1056699, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
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; SEQ ID NO 1056699
; LENGTH: 22
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-1056699

Query Match          63.3%; Score 15.2; DB 11; Length 22;
Best Local Similarity 80.0%; Pred. No. 4.1e+03;
Matches 16; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY      2 GAGAGGGGCGUGUUAAGGCG 21
        ||||| ||||| ||||| |||||
Db      21 GAGAAGGGCTGGAGAAGGCG 2

RESULT 15
US-10-310-914A-594065
; Sequence 594065, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 594065
; LENGTH: 24
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-594065

Query Match          63.3%; Score 15.2; DB 11; Length 24;
Best Local Similarity 85.0%; Pred. No. 4.1e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      2 GAGAGGGGCGUGUUAAGGCG 21
        ||||| ||||| ||||| |||||
Db      4 GAGAGGGGCGUGUUGGGGUG 23

Search completed: October 16, 2006, 16:22:41
Job time : 338.985 secs
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OM nucleic - nucleic search, using sw model

Run on: October 16, 2006, 14:16:55 ; Search time 53.2331 Seconds
(without alignments)
842.395 Million cell updates/sec

Title: US-10-604-726A-6034

Perfect score: 24

Sequence: 1 ugagagggcguuagcgucc 24

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 2395520 seqs, 934235491 residues

Total number of hits satisfying chosen parameters: 3125932

Minimum DB seq length: 0

Maximum DB seq length: 30

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications_NA_New.*

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- 2: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US06_NEW_PUB.seq.*
- 3: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US07_NEW_PUB.seq.*
- 4: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US08_NEW_PUB.seq.*
- 5: /EMC_Celerra_SIDS3/ptodata/2/pubpna/PCT_NEW_PUB.seq.*
- 6: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10_NEW_PUB.seq.*
- 7: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11_NEW_PUB.seq.*
- 8: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11_NEW_PUB.seq.*
- 9: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11_NEW_PUB.seq.*
- 10: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US60_NEW_PUB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	13.8	57.5	25	8	US-11-217-529-40910 Sequence 40910, A
C 2	13.4	55.8	25	8	US-11-217-529-25472 Sequence 25472, A
C 3	13.4	55.8	25	8	US-11-217-529-101402 Sequence 101402, A
C 4	13.2	55.0	25	8	US-11-217-529-36679 Sequence 36679, A
C 5	13.2	55.0	25	9	US-11-348-413-792144 Sequence 792144, A
C 6	13.2	55.0	25	9	US-11-348-413-877012 Sequence 877012, A
C 7	13	54.2	25	8	US-11-217-529-29983 Sequence 29983, A
C 8	13	54.2	25	8	US-11-217-529-41374 Sequence 41374, A
C 9	13	54.2	25	8	US-11-217-529-88277 Sequence 88277, A
C 10	12.8	53.3	25	8	US-11-217-529-45581 Sequence 45581, A
C 11	12.8	53.3	25	8	US-11-217-529-111977 Sequence 111977, A
C 12	12.8	53.3	25	9	US-11-217-529-177967 Sequence 177967, A
C 13	12.8	53.3	25	9	US-11-348-413-32918 Sequence 32918, A
C 14	12.8	53.3	25	9	US-11-348-413-32919 Sequence 32919, A
C 15	12.8	53.3	25	9	US-11-348-413-32920 Sequence 32920, A
C 16	12.8	53.3	25	9	US-11-348-413-32921 Sequence 32921, A
C 17	12.8	53.3	25	9	US-11-348-413-620816 Sequence 620816, A
C 18	12.8	53.3	25	9	US-11-348-413-620817 Sequence 620817, A
C 19	12.8	53.3	25	9	US-11-348-413-620818 Sequence 620818, A
C 20	12.8	53.3	25	9	US-11-348-413-1233237 Sequence 1233237, A
C 21	12.6	52.5	25	8	US-11-217-529-74782 Sequence 74782, A
C 22	12.6	52.5	25	8	US-11-217-529-113852 Sequence 113852, A
C 23	12.6	52.5	25	9	US-11-348-413-657889 Sequence 657889, A

C 24	12.6	52.5	25	9	US-11-348-413-697258 Sequence 697258, A
C 25	12.6	52.5	25	9	US-11-348-413-815414 Sequence 815414, A
C 26	12.4	51.7	25	8	US-11-217-529-25937 Sequence 25937, A
C 27	12.4	51.7	25	8	US-11-217-529-91282 Sequence 91282, A
C 28	12.4	51.7	25	8	US-11-217-529-112070 Sequence 112070, A
C 29	12.4	51.7	25	8	US-11-217-529-135665 Sequence 135665, A
C 30	12.4	51.7	25	8	US-11-217-529-135070 Sequence 135070, A
C 31	12.4	51.7	25	8	US-11-217-529-136635 Sequence 136635, A
C 32	12.4	51.7	25	8	US-11-217-529-190002 Sequence 190002, A
C 33	12.4	51.7	25	9	US-11-348-413-130141 Sequence 130141, A
C 34	12.4	51.7	25	9	US-11-348-413-130142 Sequence 130142, A
C 35	12.4	51.7	25	9	US-11-348-413-152231 Sequence 152231, A
C 36	12.4	51.7	25	9	US-11-348-413-152232 Sequence 152232, A
C 37	12.4	51.7	25	9	US-11-348-413-365681 Sequence 365681, A
C 38	12.4	51.7	25	9	US-11-348-413-365682 Sequence 365682, A
C 39	12.4	51.7	25	9	US-11-348-413-365683 Sequence 365683, A
C 40	12.4	51.7	25	9	US-11-348-413-612898 Sequence 612898, A
C 41	12.4	51.7	25	9	US-11-348-413-666212 Sequence 666212, A
C 42	12.4	51.7	25	9	US-11-348-413-680583 Sequence 680583, A
C 43	12.4	51.7	25	9	US-11-348-413-681934 Sequence 681934, A
C 44	12.4	51.7	25	9	US-11-348-413-724848 Sequence 724848, A
C 45	12.4	51.7	25	9	US-11-348-413-724849 Sequence 724849, A

ALIGNMENTS.

RESULT 1
US-11-217-529-40910/c
; Sequence 40910, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 40910
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-40910

Query Match 57.5%; Score 13.8; DB 8; Length 25;
Best Local Similarity 70.6%; Pred. No. 4.1e+03;
Matches 12; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 8 GGCUGGUUAAAGCGGUCC 24
|||||:|||||
DB 24 GGCCTGTTAAAGCGGCC 8

RESULT 2
US-11-217-529-25472
; Sequence 25472, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS

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; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 25472
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-25472

Query Match          55.8%; Score 13.4; DB 8; Length 25;
Best Local Similarity 66.7%; Pred. No. 6.3e+03;
Matches 10; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 9 GCGUGUUAAGCGC 23
   |||:|:|:|:|:|
Db 9 GCTGGTTAGCGTC 23

RESULT 3
US-11-217-529-101402/c
; Sequence 101402, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 101402
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-101402

Query Match          55.8%; Score 13.4; DB 8; Length 25;
Best Local Similarity 56.5%; Pred. No. 6.3e+03;
Matches 13; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 1 UGAGAGGCGGUGUUAAGCGC 23
   |||:|:|:|:|:|
Db 24 TGAGACGGGTAGTTAAGTAGAC 2

RESULT 4
US-11-217-529-36679/c
; Sequence 36679, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
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; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 36679
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-36679

Query Match          55.0%; Score 13.2; DB 8; Length 25;
Best Local Similarity 66.7%; Pred. No. 7.8e+03;
Matches 12; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 3 AGAGGGCGUGGUUAAGGC 20
   |||:|:|:|:|:|
Db 25 ATAGGGCCTGGTTAAAGC 8

RESULT 5
US-11-348-792144
; Sequence 792144, Application US/11348413
; Publication No. US20060160121A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; APPLICANT: Murphy, Ellen
; APPLICANT: Olmsted, Stephen
; TITLE OF INVENTION: PROBE ARRAYS FOR DETECTING MULTIPLE STRAINS OF DIFFERENT SPECIES
; FILE REFERENCE: 031896-084100 (AM 101724)
; CURRENT APPLICATION NUMBER: US/11/348,413
; CURRENT FILING DATE: 2006-02-07
; PRIOR APPLICATION NUMBER: PCT/US05/035471
; PRIOR FILING DATE: 2005-10-05
; PRIOR APPLICATION NUMBER: US 11/243,445
; PRIOR FILING DATE: 2005-10-05
; PRIOR APPLICATION NUMBER: US 60/615,573
; PRIOR FILING DATE: 2004-10-05
; NUMBER OF SEQ ID NOS: 1276209
; SEQ ID NO 792144
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: probe
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)-(25)
; OTHER INFORMATION: SEQ ID NO: 5316; WAN01UNLH_at; Start 930; Stop 954;
; OTHER INFORMATION: 0000100000000000
US-11-348-792144

Query Match          55.0%; Score 13.2; DB 9; Length 25;
Best Local Similarity 66.7%; Pred. No. 7.8e+03;
Matches 12; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 5 AGGGGCGUGGUUAAGCGU 22
   |||:|:|:|:|:|
Db 5 AAGGGCTGGTATAGGCGT 22

RESULT 6
US-11-348-413-877012/c
; Sequence 877012, Application US/11348413
; Publication No. US20060160121A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; APPLICANT: Murphy, Ellen
; APPLICANT: Olmsted, Stephen
; TITLE OF INVENTION: PROBE ARRAYS FOR DETECTING MULTIPLE STRAINS OF DIFFERENT SPECIES
; FILE REFERENCE: 031896-084100 (AM 101724)
; CURRENT APPLICATION NUMBER: US/11/348,413
; CURRENT FILING DATE: 2006-02-07
; PRIOR APPLICATION NUMBER: PCT/US05/035471
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; PRIOR FILING DATE: 2005-10-05
; PRIOR APPLICATION NUMBER: US 11/243,445
; PRIOR FILING DATE: 2005-10-05
; PRIOR APPLICATION NUMBER: US 60/615,573
; PRIOR FILING DATE: 2004-10-05
; NUMBER OF SEQ ID NOS: 1276209
; SEQ ID NO 877012
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: probe
; NAME/KEY: misc feature
; LOCATION: (1)..(25)
; OTHER INFORMATION: SEQ ID NO: 7631; WANOLUMIA_at; Start 143; Stop 167;
; OTHER INFORMATION: 00000011100000
US-11-348-413-877012

Query Match      55.0%; Score 13.2; DB 9; Length 25;
Best Local Similarity 72.2%; Pred. No. 7.8e+03;
Matches 13; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY      3 AGAGGGCGUGGUUAGGCG 20
Db      23 AGATGGCCGATTAAAGC 6

RESULT 7
US-11-217-529-29983/c
; Sequence 29983, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 29983
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-29983

Query Match      54.2%; Score 13; DB 8; Length 25;
Best Local Similarity 57.1%; Pred. No. 9.6e+03;
Matches 12; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY      3 AGAGGGCGUGGUUAGGCGUC 23
Db      25 AGAGGGCGTGTTCCTCTTC 5

RESULT 8
US-11-217-529-41374
; Sequence 41374, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 41374
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-41374

Query Match      54.2%; Score 13; DB 8; Length 25;
Best Local Similarity 57.1%; Pred. No. 9.6e+03;
Matches 12; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY      3 AGAGGGCGUGGUUAGGCGUC 23
Db      4 AAAGTGGCTGTTCAGGATTC 24

RESULT 9
US-11-217-529-88277
; Sequence 88277, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 88277
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-88277

Query Match      54.2%; Score 13; DB 8; Length 25;
Best Local Similarity 57.1%; Pred. No. 9.6e+03;
Matches 12; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY      3 AGAGGGCGUGGUUAGGCGUC 23
Db      4 AAAGTGGCTGTTCAGGATTC 24

RESULT 10
US-11-217-529-45581
; Sequence 45581, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
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; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 45581
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-45581

Query Match      53.3%; Score 12.8; DB 8; Length 25;
Best Local Similarity 75.0%; Pred. No. 1.2e+04;
Matches 12; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY      4 GAGGGCGUGGUUAGG 19
        |||||:||||:|
Db       6 GAGGGAAGTGTCAAG 21

RESULT 11
US-11-217-529-111977/c
; Sequence 111977, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHITIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIOHKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 111977
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-111977

Query Match      53.3%; Score 12.8; DB 8; Length 25;
Best Local Similarity 54.2%; Pred. No. 1.2e+04;
Matches 13; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

QY      1 UGAGAGGGCGUGGUUAGGCGUCC 24
        :|||||:||||:|
Db      24 TGAGAAACGCTAGTAAACGCATCC 1

RESULT 12
US-11-217-529-177967/c
; Sequence 177967, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHITIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIOHKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 177967
; LENGTH: 25
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; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-177967

Query Match      53.3%; Score 12.8; DB 8; Length 25;
Best Local Similarity 62.5%; Pred. No. 1.2e+04;
Matches 10; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY      8 GCGUGGUUAGGCGUC 23
        |||:||||:|
Db       22 GGTTCGTTAAGGCATC 7

RESULT 13
US-11-348-413-32918
; Sequence 32918, Application US/11348413
; Publication No. US20060160121A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; APPLICANT: Murphy, Ellen
; APPLICANT: Olmsted, Stephen
; TITLE OF INVENTION: PROBE ARRAYS FOR DETECTING MULTIPLE STRAINS OF DIFFERENT SPECIES
; FILE REFERENCE: 031896-084100 (AM 101724)
; CURRENT APPLICATION NUMBER: US/11/348,413
; CURRENT FILING DATE: 2006-02-07
; PRIOR APPLICATION NUMBER: PCT/US05/035471
; PRIOR FILING DATE: 2005-10-05
; PRIOR APPLICATION NUMBER: US 11/243,445
; PRIOR FILING DATE: 2005-10-05
; PRIOR APPLICATION NUMBER: US 60/615,573
; NUMBER OF SEQ ID NOS: 1276209
; SEQ ID NO 32918
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: probe
; NAME/KEY: misc_feature
; LOCATION: (1)..(25)
; OTHER INFORMATION: SEQ ID NO: 423; WAN01UJBU; Start 271; Stop 295;
; OTHER INFORMATION: 111111100000000
US-11-348-413-32918

Query Match      53.3%; Score 12.8; DB 9; Length 25;
Best Local Similarity 62.5%; Pred. No. 1.2e+04;
Matches 10; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY      1 UGAGAGGGCGUGGUUA 16
        :|||||:||||:|
Db       9 TAAAGACGGCTGTTA 24

RESULT 14
US-11-348-413-32919
; Sequence 32919, Application US/11348413
; Publication No. US20060160121A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; APPLICANT: Murphy, Ellen
; APPLICANT: Olmsted, Stephen
; TITLE OF INVENTION: PROBE ARRAYS FOR DETECTING MULTIPLE STRAINS OF DIFFERENT SPECIES
; FILE REFERENCE: 031896-084100 (AM 101724)
; CURRENT APPLICATION NUMBER: US/11/348,413
; CURRENT FILING DATE: 2006-02-07
; PRIOR APPLICATION NUMBER: PCT/US05/035471
; PRIOR FILING DATE: 2005-10-05
; PRIOR APPLICATION NUMBER: US 11/243,445
; PRIOR FILING DATE: 2005-10-05
; PRIOR APPLICATION NUMBER: US 60/615,573
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; PRIOR FILING DATE: 2004-10-05
; NUMBER OF SEQ ID NOS: 1276209
; SEQ ID NO 32919
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: probe
; NAME/KEY: misc feature
; LOCATION: (1)..(25)
; OTHER INFORMATION: SEQ ID NO: 423; WAN01UJBU; Start 272; Stop 296;
; OTHER INFORMATION: 11111100000000
US-11-348-413-32919

Query Match 53.3%; Score 12.8; DB 9; Length 25;
Best Local Similarity 62.5%; Pred. No. 1.2e+04;
Matches 10; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 UGAGAGGGCGUGGUUA 16
: ||| |||||:|:
Db 8 TAAGACGGGCTGGTTA 23

RESULT 15
US-11-348-413-32920
; Sequence 32920, Application US/11348413
; Publication No. US20060160121A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; APPLICANT: Murphy, Ellen
; APPLICANT: Olmsted, Stephen
; TITLE OF INVENTION: PROBE ARRAYS FOR DETECTING MULTIPLE STRAINS OF DIFFERENT SPECIES
; FILE REFERENCE: 031896-084100 (AM 101724)
; CURRENT APPLICATION NUMBER: US/11/348,413
; CURRENT FILING DATE: 2006-02-07
; PRIOR APPLICATION NUMBER: PCT/US05/035471
; PRIOR FILING DATE: 2005-10-05
; PRIOR APPLICATION NUMBER: US 11/243,445
; PRIOR FILING DATE: 2005-10-05
; PRIOR APPLICATION NUMBER: US 60/615,573
; PRIOR FILING DATE: 2004-10-05
; NUMBER OF SEQ ID NOS: 1276209
; SEQ ID NO 32920
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: probe
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(25)
; OTHER INFORMATION: SEQ ID NO: 423; WAN01UJBU; Start 273; Stop 297;
; OTHER INFORMATION: 11111100000000
US-11-348-413-32920

Query Match 53.3%; Score 12.8; DB 9; Length 25;
Best Local Similarity 62.5%; Pred. No. 1.2e+04;
Matches 10; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 UGAGAGGGCGUGGUUA 16
: ||| |||||:|:
Db 7 TAAGACGGGCTGGTTA 22

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OM nucleic - nucleic search, using sw model

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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
C 1	27.8	11.0	98	5	S69137	S69137 Homo sapien
C 2	26.2	10.4	98	5	S69198	S69198 Homo sapien
C 3	25.2	10.0	109	7	AB150733	AB150733 Homo sapi
C 4	24.8	9.8	92	2	BD035734	BD035734 Sequence
C 5	24.8	9.8	92	2	AR735995	AR735995 Sequence
C 6	24.8	9.8	92	2	AX900201	AX900201 Sequence
C 7	24.6	9.8	103	2	CQ471292	CQ471292 Sequence
C 8	24.6	9.8	104	2	CQ480460	CQ480460 Sequence
C 9	24.4	9.7	119	5	AY751306	AY751306 Homo sapi
C 10	24.2	9.6	96	2	AR431314	AR431314 Sequence
C 11	23.8	9.4	78	2	AR477180	AR477180 Sequence
C 12	23.8	9.4	78	2	AR606935	AR606935 Sequence
C 13	23.8	9.4	78	2	AR701924	AR701924 Sequence
C 14	23.6	9.4	72	2	BD034735	BD034735 Sequence
C 15	23.6	9.4	72	2	AR734996	AR734996 Sequence
C 16	23.6	9.4	72	2	AX899202	AX899202 Sequence
C 17	23.6	9.4	97	2	AX184498	AX184498 Sequence
C 18	23.4	9.3	100	2	AX989552	AX989552 Sequence

19	23.4	9.3	100	2	AX996400	AX996400 Sequence
20	23.4	9.3	100	2	CQ874706	CQ874706 Sequence
C 21	23.2	9.2	59	2	E37929	E37929 Remedy for
C 22	23.2	9.2	81	10	AY390010	AY390010 Hepatitis
C 23	23.2	9.2	101	2	CQ149122	CQ149122 Sequence
C 24	23.2	9.2	101	2	CQ232396	CQ232396 Sequence
C 25	23.2	9.2	101	2	CQ307710	CQ307710 Sequence
C 26	23.2	9.2	101	2	CQ344556	CQ344556 Sequence
C 27	23.2	9.2	111	5	HSA012224	AF012224 Homo sapi
C 28	23	9.1	51	6	AF094482	AF094482 Mus muscu
C 29	23	9.1	54	6	AY177451	AY177451 Mus muscu
C 30	23	9.1	65	2	CQ531157	CQ531157 Sequence
C 31	23	9.1	81	10	AF040860	AF040860 Hepatitis
C 32	23	9.1	120	7	EV012636	EV012636 MS201 Hu
C 33	22.8	9.0	60	2	CQ546820	CQ546820 Sequence
C 34	22.8	9.0	110	5	HSRETINT11	U11537 Human RET p
C 35	22.6	9.0	66	2	CQ630945	CQ630945 Sequence
C 36	22.6	9.0	66	2	AR472008	AR472008 Sequence
C 37	22.4	8.9	60	6	MUSIGXYZ	M38077 Mouse Ig S-
C 38	22.4	8.9	98	6	AF387673	AF387673 Mesozrice
C 39	22.4	8.9	119	2	AX907922	AX907922 Sequence
C 40	22.4	8.9	119	2	BD043455	BD043455 Sequence
C 41	22.4	8.9	119	2	AR743716	AR743716 Sequence
C 42	22.2	8.8	51	2	CQ007958	CQ007958 Sequence
C 43	22.2	8.8	67	2	BD034947	BD034947 Sequence
C 44	22.2	8.8	67	2	AR735208	AR735208 Sequence
C 45	22.2	8.8	67	2	AX899414	AX899414 Sequence

ALIGNMENTS

RESULT 1	S69137/c	S69137	Homo sapiens T-cell receptor alpha-chain (TCR V alpha) mRNA, partial cds.	98 bp	mRNA	linear	PRI 16-MAR-2001
LOCUS	S69137	S69137	Homo sapiens T-cell receptor alpha-chain (TCR V alpha) mRNA, partial cds.				
DEFINITION	S69137	S69137	Homo sapiens T-cell receptor alpha-chain (TCR V alpha) mRNA, partial cds.				
ACCESSION	S69137	S69137	Homo sapiens (human)				
VERSION	S69137.1	GI:545967	Homo sapiens (human)				
KEYWORDS							
SOURCE			Homo sapiens (human)				
ORGANISM			Homo sapiens				
REFERENCE			1 (bases 1 to 98)				
AUTHORS			Mohapatra,S.S., Mohapatra,S., Yang,M., Ansari,A.A., Patronchi,P., Maggi,E. and Romagnani,S.				
TITLE			Molecular basis of cross-reactivity among allergen-specific human T cells: T-cell receptor V alpha gene usage and epitope structure				
JOURNAL			Immunology 81 (1), 15-20 (1994)				
PUBMED			7510663				
REMARK			GenBank staff at the National Library of Medicine created this entry [NCBI gibbon 144559] from the original journal article.				
FEATURES			Location/Qualifiers				
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			/organism="Homo sapiens"				
			/mol_type="mRNA"				
			/isolate="grass-sensitive individual VI 24"				
			/db_xref="taxon:9606"				
			/tissue_type="peripheral blood"				
gene			<1..>98				
			/gene="TCR V alpha"				
CDS			<1..>98				
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			/note="allergen-specific; mismatch(30 [D->N]) when compared with sequence in paper"				
			/codon_start=1				
			/product="T-cell receptor alpha-chain"				
			/protein_id="AAB30241.2"				
			/db_xref="GI:13366254"				
			/translation="DSATYFCAASTNACKSTFGSGTTLTVKPNIQ"				
ORIGIN							

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Best Local Similarity	57.5%;	Pred. No. 1.9e+03;		
Matches 50;	Conservative 0;	Mismatches 37;	Indels 0;	Gaps 0;
QY	65	GTTCCTGAGTGCAGAGTCTCTGACTCCCTCTGCCACGGCTGAGTTCCCGGCTCCAGG 124		
Db	93	GATATTGGCTTCACAGTGAGCGTAGTCCCACTCCCAAGGTTGATTGCCTGCATTGGT 34		
QY	125	TTCCGCGTGCCTGAGGTTTGAGGC 151		
Db	33	GGTGCTTGCTGCACAGAGTAGGTGGC 7		
RESULT 2				
S69198/c				
LOCUS	S69198	98 bp	mRNA	linear PRI 06-MAR-2001
DEFINITION	Homo sapiens T-cell receptor alpha-chain (TCR V alpha) mRNA, partial cds.			
ACCESSION	S69198			
VERSION	S69198.1	GI:545963		
KEYWORDS	Homo sapiens (human)			
SOURCE	Homo sapiens			
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominiidae; Homo.			
REFERENCE	1 (bases 1 to 98)			
AUTHORS	Mohapatra,S.S., Mohapatra,S., Yang,M., Ansari,A.A., Parronchi,P., Maggi,E. and Romagnani,S.			
TITLE	Molecular basis of cross-reactivity among allergen-specific human T cells: T-cell receptor V alpha gene usage and epitope structure			
JOURNAL	Immunology 81 (1), 15-20 (1994)			
PUBMED	7510663			
REMARK	GenBank staff at the National Library of Medicine created this entry [NCBI Gibbsq 144557] from the original journal article.			
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source	1..98			
	/organism="Homo sapiens"			
	/mol_type="mRNA"			
	/isolates="grass-sensitive individual VI 17"			
	/db_xref="taxon:9606"			
gene	/tissue_type="peripheral blood"			
	<1..>98			
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	/db_xref="GI:13236916"			
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Best Local Similarity	56.3%;	Pred. No. 6.2e+03;		
Matches 49;	Conservative 0;	Mismatches 38;	Indels 0;	Gaps 0;
QY	65	GTTCCTGAGTGCAGAGTCTCTGACTCCCTCTGCCACGGCTGAGTTCCCGGCTCCAGG 124		
Db	93	GATATTGGCTTCACAGTGAGCGTAGTCCCACTCCCAAGGTTGATTGCCTGCATTGGT 34		
QY	125	TTCCGCGTGCCTGAGGTTTGAGGC 151		
Db	33	GGTGCTTGCTGCACAGAGTAGGTGGC 7		
RESULT 3				
AB150733				
LOCUS	AB150733	109 bp	DNA	linear STS 27-OCT-2005
DEFINITION	Homo sapiens DNA, STS on chromosome 10, D10S08121, sequence tagged site.			
ACCESSION	AB150733			

VERSION	AB150733.1	GI:62171551		
KEYWORDS	STS.			
SOURCE	Homo sapiens (human)			
ORGANISM	Homo sapiens			
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominiidae; Homo.			
REFERENCE	1			
AUTHORS	Tamiya,G., Shinya,M., Imanishi,T., Ikuta,T., Makino,S., Okamoto,K., Furugaki,K., Matsumoto,T., Mano,S., Ando,S., Nozaki,Y., Yukawa,W., Nakashige,R., Yamaguchi,D., Ishibashi,H., Yonekura,M., Nakami,Y., Takayama,S., Endo,T., Saruwatari,T., Yagura,M., Yoshikawa,Y., Fujimoto,K., Oka,A., Chiku,S., Linsen,S.E., Giphart,M.J., Kuleki,J.K., Fukazawa,T., Hashimoto,H., Kimura,M., Hoshina,Y., Suzuki,Y., Hotta,T., Mochida,J., Minezaki,T., Komai,K., Shiozawa,S., Taniguchi,A., Yamanaka,H., Kamatani,N., Gojobori,T., Bahram,S. and Inoko,H.			
TITLE	Whole genome association study of rheumatoid arthritis using 27 039 microsatellites			
JOURNAL	Hum. Mol. Genet. 14 (16), 2305-2321 (2005)			
PUBMED	16000323			
REFERENCE	2 (bases 1 to 109)			
AUTHORS	Tamiya,G., Makino,S., Fujimoto,K., Oka,A., Hayashi,H., Denda,A., Linsen,S.E., Ikuta,T., Shinya,M., Endo,T., Tomizawa,M., Tokubo,E., Sato,R., Takaki,A., Nagatsuka,Y., Watanabe,H., Adachi,S., Makino,Y., Nakano,S., Yamamoto,A., Yoshida,K., Okamoto,K., Yamaguchi,D., Ishibashi,H., Yonekura,M., Takayama,S., Nakami,Y., Saruwatari,T., Brand,A., van Hilten,J.A., van de Watering,L.M., Giphart,M.J., Bahram,S., Kuleki,Y.J. and Inoko,H.			
TITLE	Direct Submission			
JOURNAL	Submitted (12-DEC-2003) Hidetoshi Inoko, Tokai University School of Medicine, Department of Genetic Information, Bohseidai, Isehara, Kanagawa, 259-1193, Japan [E-mail:hinoko@is.icc.u-tokai.ac.jp, Tel:81-463-93-1121, Fax:81-463-94-8884]			
COMMENT	Polymorphisms were confirmed by comparing with the pooled DNA typing data of 88 Dutch population or 100 Australian. When there was no significant difference between the Japanese and these Caucasians, individual typing was performed to confirm polymorphisms.			
FEATURES	Location/Qualifiers			
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	/organism="Homo sapiens"			
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	/db_xref="taxon:9606"			
	/chromosome="10"			
	/map="10q23.2"			
primer_bind	/note="5' primer: TCATGACAGGTGGTAGG"			
	1..18			
	/PCR_conditions="denaturation 96degC 5 min, 57degC 1 min, 72degC 1 min; 40 cycles 96degC 45 sec, 57degC 45 sec, 72degC 1 min"			
repeat_region	51..78			
	/note="sequence tagged site D10S08121"			
	/rpt_type=tandem			
	/rpt_unit_seq="cagg"			
primer_bind	complement(189..109)			
	/note="3' primer: TCAGGAAGGTGCTGTACTCTC"			
ORIGIN				
Query Match	10.0%;	Score 25.2;	DB 7;	Length 109;
Best Local Similarity	62.9%;	Pred. No. 1.3e+04;		
Matches 39;	Conservative 0;	Mismatches 23;	Indels 0;	Gaps 0;
QY	138	CTGAGGTTTGAGGCCAGACAGCTCGCAGTCGGGCGAGGAGGGCGGGGAGACGAGCGG 197		
Db	42	CTGAGTTTTCAGGCAGGCAGGCAGGCAGGCAGGCAGGCAGGCAGGCAGGCAGGCAG 101		
QY	198	CT 199		
Db	102	CT 103		

Query Match	9.8%; Score 24.8; DB 2;	Length 92;
Best Local Similarity	67.3%; Pred. No. 1.7e+04;	
Matches	35; Conservative	0; Mismatches 17; Indels 0; Gaps 0;

Qy	156	CAGCTCGCACTGGGACGAGCGGCGGGGAGACGAGCGGTCTGGCCCC	207
Db	13	CAGCTGAATCGAGCGGAACAGCGGGGCTGGAGCGCGCGGCCCCC	64

RESULT 5			PAT 11-OCT-2005
AR735995			
LOCUS	AR735995	92 bp DNA	linear
DEFINITION	Sequence 16064 from patent US 6783961.		
ACCESSION	AR735995		
VERSION	AR735995.1	GI:77429735	
KEYWORDS	Unknown.		
SOURCE	Unknown.		
ORGANISM	Unclassified.		
REFERENCE	1 (bases 1 to 92)		
AUTHORS	Edwards,J.-B.D.M., Duclert,A. and Giordano,J.-Y.		
TITLE	Expressed sequence tags and encoded human proteins		
JOURNAL	Patent: US 6783961-A 16064 31-AUG-2004;		
	Genset S.A.;;		
PRX;			

FEATURES	Location/Qualifiers
source	1..92 /organism="unknown" /mol_type="genomic DNA"

ORIGIN	
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Query Match	9.8%; Score 24.8; DB 2;	Length 92;
Best Local Similarity	67.3%; Pred. No. 1.7e+04;	
Matches	35; Conservative	0; Mismatches 17; Indels 0; Gaps 0;

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Db      62 CTCTTCCTTCGCTAACGCC 80

RESULT 8
CQ480460
LOCUS      104 bp      DNA      linear      PAT 30-JAN-2004
DEFINITION Sequence 12327 from Patent WO0160860.
ACCESSION CQ480460
VERSION    CQ480460.1 GI:41446079
KEYWORDS   .
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Homnidae; Homo.
REFERENCE  1
AUTHORS    Schlegel,R., Endege,W.O. and Monahan,J.E.
TITLE      Genes differentially expressed in human prostate cancer and their
JOURNAL    use
            Schlengel,R., Endege,W.O. and Monahan,J.E.
            Genes differentially expressed in human prostate cancer and their
            use
JOURNAL    WO 0160860-A 12327 23-AUG-2001;
            Millennium Predictive Medicine, Inc. (US)
FEATURES   Location/Qualifiers
            source          1..104
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                        /mol_type="unassigned DNA"
                        /db_xref="taxon:9606"
ORIGIN
Query Match      9.8%; Score 24.6; DB 2; Length 104;
Best Local Similarity 57.0%; Pred. No. 2e+04;
Matches 45; Conservative 0; Mismatches 34; Indels 0; Gaps 0;

QY 174 GGAGGCGGGGAGACAGAGCGCTCTGCGCCCTTAATGTACTTCGGGCTCGATTCT 233
      || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 2 GGTACGCGGGGAGACGCGCGCGCTCGACGCTGTAGTGCTTTCGCTTCGGGTTT 61
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 234 CTCTCCTTCGCGCACTCC 252
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 62 CTCTTCCTTCGCTAACGCC 80

RESULT 9
AY751306
LOCUS      119 bp      mRNA      linear      PRI 19-MAY-2005
DEFINITION Homo sapiens clone RW33 T cell receptor beta chain mRNA, partial
            cds.
ACCESSION AY751306
VERSION    AY751306.1 GI:54111802
KEYWORDS   .
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Homnidae; Homo.
REFERENCE  1 (bases 1 to 119)
AUTHORS    Barcy,S., Huang,M.L., Corey,L. and Koelle,D.M.
TITLE      Longitudinal Analysis of Herpes Simplex Virus-Specific CD4+ Cell
            Clonotypes in Infected Tissues and Blood
JOURNAL    J. Infect. Dis. 191 (12), 2012-2021 (2005)
PUBMED     15897986
REFERENCE  2 (bases 1 to 119)
AUTHORS    Barcy,S.
TITLE      Direct Submission
            Submitted (14-SEP-2004) Laboratory Medicine, University of
            Washington, 1959 N.E. Pacific Street, Rosen Bldg, Room 154,
            Seattle, WA 98109, USA
JOURNAL
FEATURES   Location/Qualifiers
            source          1..119
                        /organism="Homo sapiens"
                        /mol_type="mRNA"
                        /db_xref="taxon:9606"
                        /clone="RW33"
                        /cell_type="Herpes simplex virus specific CD4+ T

lymphocyte"
/tissue_type="herpetic skin lesion"
<1..>119
/codon_start=1
/product="T cell receptor beta chain"
/protein_id="AAV28660.1"
/db_xref="GI:54111803"
/translation="NVNALLGLDSALYLCASSSGTPYGYTFGSGTRLTVEDL"

CDS
ORIGIN
Query Match      9.7%; Score 24.4; DB 5; Length 119;
Best Local Similarity 54.4%; Pred. No. 2.4e+04;
Matches 49; Conservative 0; Mismatches 41; Indels 0; Gaps 0;

QY 37 CCCCAAGTTGGGAAGCGCTTTGCTTCTGTTTCTGGATGCAGAGTCCTCTGACTCCCTC 96
      || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 9 CGCCTTGTTGCTGGGGGACTCGGCCCTTATCTCTGCGGCACAGTTCGGGACACCTTA 68
      || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 97 TGCCACGGGCTGAGTTTTCGGGCTCCAGGTT 126
      || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 69 TGGCTACACCTTCGGTTCGGGGACCAAGTT 98
      || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 10
AR431314
LOCUS      96 bp      DNA      linear      PAT 18-DEC-2003
DEFINITION Sequence 1 from patent US 6651010.
ACCESSION AR431314
VERSION    AR431314.1 GI:40193289
KEYWORDS   .
SOURCE     Unknown.
ORGANISM   Unclassified.
            Han,K., Kim,D. and Kim,H.-J.
            Vector-based method for visualizing secondary structure of RNA
            molecules
            Patent: US 6651010-A 1 18-NOV-2003;
            INHA University Foundation; Incheon-si,
            KRX;
            Location/Qualifiers
            source          1..96
                        /organism="unknown"
                        /mol_type="unassigned DNA"
ORIGIN
Query Match      9.6%; Score 24.2; DB 2; Length 96;
Best Local Similarity 59.4%; Pred. No. 2.7e+04;
Matches 41; Conservative 0; Mismatches 28; Indels 0; Gaps 0;

QY 32 GCGCTCCCAAGTTGGAAGGCGCTTGTGCTTCTGTTTCTGGATGCAGAGTCCTCTGACT 91
      || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 10 GCGGCTGGAATCGAATTCGCTGTGCTCTCTGTCTACGCGCTGTGCTGGCTGACTGCCT 69
      || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 92 CCCTCTGCC 100
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 70 GCTGCTGCC 78
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 11
AR477180/c
LOCUS      78 bp      DNA      linear      PAT 14-MAY-2004
DEFINITION Sequence 145 from patent US 6696256.
ACCESSION AR477180
VERSION    AR477180.1 GI:47234454
KEYWORDS   .
SOURCE     Unknown.
ORGANISM   Unclassified.
            Li,X.
            Method, array and kit for detecting activated transcription factors
            by hybridization array
```



```
JOURNAL Patent: US 6696256-A 145 24-FEB-2004;
FEATURES Location/Qualifiers
source
1. .78
/organism="unknown"
/mol_type="genomic DNA"
ORIGIN
Query Match 9.4%; Score 23.8; DB 2; Length 78;
Best Local Similarity 59.7%; Pred. No. 3.5e+04;
Matches 40; Conservative 0; Mismatches 27; Indels 0; Gaps 0;
QY 109 AGTTTCGGCTCCAGGTTCCGCTGTCGCCCTGAGGTTTGAGGCCACACAGCTCGCAGTCG 168
DB 78 AGCTTCAGGTCAGAGGTCAGAGAGTAGCTTCAGGTCAGAGGTCAGAGAGCTAGCTTCAG 19
QY 169 GGCAGGG 175
DB 18 GTCAGAG 12
RESULT 12
AR606935/c
LOCUS 78 bp DNA linear PAT 15-DEC-2004
DEFINITION Sequence 145 from patent US 6821737.
ACCESSION AR606935
VERSION AR606935.1 GI:56659110
KEYWORDS Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 78)
AUTHORS Li, X.
TITLE Method for screening for drug candidates for modulating
transcription factor activity
JOURNAL Patent: US 6821737-A 145 23-NOV-2004;
Panomics, Inc.; Redwood City, CA
FEATURES Location/Qualifiers
source
1. .78
/organism="unknown"
/mol_type="genomic DNA"
ORIGIN
Query Match 9.4%; Score 23.8; DB 2; Length 78;
Best Local Similarity 59.7%; Pred. No. 3.5e+04;
Matches 40; Conservative 0; Mismatches 27; Indels 0; Gaps 0;
QY 109 AGTTTCGGCTCCAGGTTCCGCTGTCGCCCTGAGGTTTGAGGCCACACAGCTCGCAGTCG 168
DB 78 AGCTTCAGGTCAGAGGTCAGAGAGTAGCTTCAGGTCAGAGGTCAGAGAGCTAGCTTCAG 19
QY 169 GGCAGGG 175
DB 18 GTCAGAG 12
RESULT 13
AR701924/c
LOCUS 78 bp DNA linear PAT 20-SEP-2005
DEFINITION Sequence 145 from patent US 6924113.
ACCESSION AR701924
VERSION AR701924.1 GI:75917786
KEYWORDS Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 78)
AUTHORS Li, X.
TITLE Method and kit for isolating DNA probes that bind to activated
transcription factors
JOURNAL Patent: US 6924113-A 145 02-AUG-2005;
Panomics, Inc.; Redwood City, CA
FEATURES Location/Qualifiers
source
1. .78
/organism="unknown"
/mol_type="genomic DNA"
ORIGIN
Query Match 9.4%; Score 23.8; DB 2; Length 78;
Best Local Similarity 59.7%; Pred. No. 3.5e+04;
Matches 40; Conservative 0; Mismatches 27; Indels 0; Gaps 0;
QY 109 AGTTTCGGCTCCAGGTTCCGCTGTCGCCCTGAGGTTTGAGGCCACACAGCTCGCAGTCG 168
DB 78 AGCTTCAGGTCAGAGGTCAGAGAGTAGCTTCAGGTCAGAGGTCAGAGAGCTAGCTTCAG 19
QY 169 GGCAGGG 175
DB 18 GTCAGAG 12
RESULT 14
BD034735/c
LOCUS 72 bp DNA linear PAT 27-AUG-2002
DEFINITION Sequence tag and encoded human protein.
ACCESSION BD034735
VERSION BD034735.1 GI:22576477
KEYWORDS JP 2001269182-A/10981.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominiidae; Homo.
REFERENCE 1 (bases 1 to 72)
AUTHORS Edwards, J. B. D. M., Duclair, E. and Jordan, J. Y.
TITLE Sequence tag and encoded human protein
JOURNAL Patent: JP 2001269182-A 10981 02-OCT-2001;
GENSET
COMMENT OS Homo sapiens (human)
PN JP 2001269182-A/10981
PD 02-OCT-2001
PF 24-FEB-2000 JP 2000118773
PI 26-FEB-1999 US 60/122487
PI JEAN BAPTISTE DUMAS MILNE EDWARDS, EIMERIC DUCLAIR, JEAN YVES
PI JORDAN
PC C12N15/09, C07K14/435, C07K16/18, C12N1/15, C12N1/19, C12N1/21, PC
C12N5/10,
PC C12P21/02, C12P21/08, C12Q1/68//G06F17/30, C12N15/00, C12N5/00, PC
G06F15/40
CC
FH Key Location/Qualifiers.
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1. .72
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
ORIGIN
Query Match 9.4%; Score 23.6; DB 2; Length 72;
Best Local Similarity 69.6%; Pred. No. 4e+04;
Matches 32; Conservative 0; Mismatches 14; Indels 0; Gaps 0;
QY 128 GCGTTCGCCCTGAGGTTTGAGGCCACAGACAGCTCGCAGTCGGGCAG 173
DB 58 GCGTGGGGCCCGGGGATCGAGGGCATCCAGGCACAGACAGAGCGGCCAG 13
RESULT 15
AR734996/c
LOCUS 72 bp DNA linear PAT 11-OCT-2005
DEFINITION Sequence 15065 from patent US 6789961.
ACCESSION AR734996
VERSION AR734996.1 GI:77428736
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unknown.
```

Unclassified.
REFERENCE 1 (bases 1 to 72)
AUTHORS Edwards J.-B.D.M., Duclert A. and Giordano J.-Y.
TITLE Expressed sequence tags and encoded human proteins
JOURNAL Patent: US 6783961-A 15065 31-AUG-2004;
Genset S.A.;;
FRX;

FEATURES
source Location/Qualifiers
1..72
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN

Query Match 9.4%; Score 23.6; DB 2; Length 72;
Best Local Similarity 69.6%; Pred. No. 4e+04;
Matches 32; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

QY 128 GCGTGTGCGCCCTGAGGTTTGAGGCCACAGAGCTCGCAGTCGGGCAG 173
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Db 58 GCGTGGGGCCCCGGGGATCGAGGGCATCCAGCACAGAGGGGCCAG 13

Search completed: October 16, 2006, 13:38:02
Job time : 1373 secs

GenCore version 5.1.9
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OM nucleic - nucleic search, using sw model

Run on: October 16, 2006, 13:10:14 ; Search time 254 Seconds
 (without alignments)
 6917.349 Million cell updates/sec

Title: US-10-604-726A-8797

Perfect score: 252

Sequence: 1 ggggtatctgcaactgagag.....tctctcttctgcccacctcc 252

Scoring table: IDENTITY NUC
 Gapop 10_0 , Gapext 1.0

Searched: 5244920 seqs, 3486124231 residues

Total number of hits satisfying chosen parameters: 5729524

Minimum DB seq length: 0

Maximum DB seq length: 120

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : N_Geneseq_8.*

- 1: Geneseqn1980s.*
- 2: Geneseqn1990s.*
- 3: Geneseqn2000s.*
- 4: Geneseqn2001as.*
- 5: Geneseqn2001bs.*
- 6: Geneseqn2002as.*
- 7: Geneseqn2002bs.*
- 8: Geneseqn2003as.*
- 9: Geneseqn2003bs.*
- 10: Geneseqn2003cs.*
- 11: Geneseqn2003ds.*
- 12: Geneseqn2004as.*
- 13: Geneseqn2004bs.*
- 14: Geneseqn2005s.*
- 15: Geneseqn2006s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	25.6	10.2	115	6	ABQ76940 Polylinke
2	24.8	9.8	92	3	AAC11989 Human sec
3	24.6	9.8	103	5	ABV03167 Human pro
4	24.6	9.8	104	5	ABV12336 Human pro
5	24.2	9.6	105	4	AAB36160 Human col
6	23.8	9.4	78	8	ABT17318 Transcrip
7	23.6	9.4	72	3	AAC10990 Human sec
8	23.6	9.4	97	4	AAB68919 Human con
9	23.4	9.3	100	8	ACD69745 E. coli K
10	23.4	9.3	100	8	ACD76587 E. coli K
11	23.4	9.3	100	13	ADR28210 Oligonucle
12	23.4	9.3	100	13	ADR99734 Nucleic a
13	23.2	9.2	59	3	AAB289260 Human emb
14	23.2	9.2	101	4	AAB44587 Human bon
15	23.2	9.2	101	4	AAB18659 Human bra
16	23.2	9.2	101	4	ABE44245 Human liv
17	23.2	9.2	101	6	ABSI1824 Human gen
18	23.2	9.2	118	12	ACH88031 Human gen

ALIGNMENTS

RESULT 1

ABQ76940
 ID ABQ76940 standard; DNA; 115 BP.

XX AC ABQ76940;

XX DT 27-MAR-2003 (first entry)

XX DE Polylinker ScaI-Li- (BsgI-ScaI) DNA.

XX KW Murine; T cell receptor; TCR; hdm2; T cell response; alpha TCR; beta TCR;
 antigen-recognition sequence; ARS; fusion construct; cytostatic;
 XX KW apoptotic; tumour; leukaemia; immunisation; ds.

OS Synthetic.

XX PN DE10109854-A1.

XX PD 12-SEP-2002.

XX PF 01-MAR-2001; 2001DE-01009854.

XX PR 01-MAR-2001; 2001DE-01009854.

XX (STAN/) STANISLAWSKI T.

XX Theobalt M, Voss H, Stanislawski T;

XX WPI; 2002-714556/78.

XX P-PSDB; ABG73655.

XX PT New polypeptide of a murine alpha/beta T-cell receptor, useful for
 treating tumors and leukemia, induces specific lysis or apoptosis of cells
 expressing hdm2 protein.

XX Example 2; Fig 6; 52pp; German.

XX CC This invention describes a novel murine alphabeta T-cell receptor (TCR)
 that mediates a hdm2 protein-specific T cell response, a fusion protein
 (FP) that includes the TCR and nucleic acid encoding it, alpha or beta-
 chains of a TCR that include the antigen-recognizing sequence (ARS) of an

ABn28044 Rat splic
 ABn175509 Corn tass
 ABn43707 Human spl
 ADg91596 Template
 Ada73750 Carcinoma
 ABn15693 Human gen
 ACn78783 Human GDM
 AAC19710 Human sec
 AAC13330 Human SNP
 AAC11202 Human sec
 ADt50936 Human mus
 ADt50937 Human mus
 ADt50938 Human mus
 AAz60564 A neubias
 ABt11892 PCR produ
 AAa46418 Ribosomal
 AAC16203 Human sec
 AC125369 DNA clone
 AEE99649 Mouse mir
 ADx04314 Mouse pri
 AAq97727 Toxoplasma
 AEB50490 Human myo
 ABA36569 Probe #15
 AAz89261 Human emb
 AC168051 M. xanthu
 ABS67407 cDNA enco
 ABS67408 Complemen


```
Db 2 GGTACCGGGGAGACCGCGCGCTGCGAGCTGTAGTGGCTTCGCTTCGGTTT 61
QY 234 CTCCTCTTTTCGGCACCTCC 252
Db 62 CTCCTCTTCGCTAAGGCC 80

RESULT 4
ID ABV12336 standard; cDNA; 104 BP.
AC ABV12336;
XX
XX
XX 13-SEP-2002 (first entry)
XX
XX Human prostate expression marker cDNA 12327.
XX
XX Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;
XX pharmacogenomic marker; gene; ss.
XX
XX Homo sapiens.
XX
XX WO200160860-A2.
XX
XX 23-AUG-2001.
XX
XX 20-FEB-2001; 2001WO-US005171.
XX
XX 17-FEB-2000; 2000US-0183319P.
XX
XX 16-MAR-2000; 2000US-0189862P.
XX
XX 25-MAY-2000; 2000US-0207454P.
XX
XX 09-JUN-2000; 2000US-0211314P.
XX
XX 18-JUL-2000; 2000US-0219007P.
XX
XX 13-DEC-2000; 2000US-0255281P.
XX
XX (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
XX
XX Schlegel R, Endege WO, Monahan JE;
XX
XX WPI; 2001-662795/76.
XX
XX Novel isolated nucleic acid molecule associated with cancerous state of
XX prostate cells and correlating with presence of prostate cancer, useful
XX for detecting presence of prostate cancer, stage of prostate cancer.
XX
XX Claim 1; Page 2030; 11750pp; English.
XX
XX The invention relates to an isolated nucleic acid molecule (I) comprising
XX a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the
XX specification or its complement. (I) is useful for: (a) assessing whether
XX a patient is afflicted with prostate cancer; (b) monitoring the
XX progression of prostate cancer in a patient; (c) assessing the efficacy
XX of a test compound to inhibit prostate cancer in a patient; (d) assessing
XX the efficacy of a therapy for inhibiting prostate cancer in a patient;
XX (e) selecting a composition for inhibiting prostate cancer in a patient;
XX (f) assessing the prostate cell carcinogenic potential of a compound; (g)
XX determining whether prostate cancer has metastasized in a patient; (h)
XX assessing the aggressiveness or indolence of prostate cancer in a patient
XX ; (I) is also useful as a pharmacodynamic or pharmacogenomic marker
XX
XX Sequence 104 BP; 9 A; 39 C; 30 G; 26 T; 0 U; 0 Other;
XX
XX Query Match 9.8%; Score 24.6; DB 5; Length 104;
XX Best Local Similarity 57.0%; Pred. No. 2.5e+03;
XX Matches 45; Conservative 0; Mismatches 34; Indels 0; Gaps 0;

QY 174 GGAGGCGGGGAGACGAGCGGCTCTGGCCCCCTTAATTGTACTTTCGGGCTCGTATTCT 233
Db 2 GGTACCGGGGAGACCGCGCGCTGCGAGGCTGTAGTGGCTTCGCTTCGGTTT 61
QY 234 CTCCTCTTTTCGGCACCTCC 252
```

```
Db 62 CTCCTCTTCGCTAAGGCC 80

RESULT 5
AAH36160
ID AAH36160 standard; cDNA; 105 BP.
XX
XX AAH36160;
AC
XX
XX 03-SEP-2001 (first entry)
XX
XX Human colon cancer antigen encoding cDNA SEQ ID NO:3242.
XX
XX Human; colon cancer; colon cancer antigen; diagnosis; detection;
XX colorectal carcinoma; ss.
XX
XX Homo sapiens.
XX
XX WO200122920-A2.
XX
XX 05-APR-2001.
XX
XX 28-SEP-2000; 2000WO-US026524.
XX
XX 29-SEP-1999; 99US-0157137P.
XX
XX 03-NOV-1999; 99US-0163280P.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX Ruben SM, Barash SC, Birse CE, Rosen CA;
XX
XX WPI; 2001-235357/24.
XX
XX P-PSDB; AAG76755.
XX
XX Nucleic acids encoding 4277 human colon cancer-associated polypeptides,
XX useful for preventing, diagnosing and/or treating colorectal cancers.
XX
XX Claim 1; Page 5034-5035; 9803pp; English..
XX
XX AAH32943 to AAH37195 and AAG73514 to AAG77788 represent human colon
XX cancer-associated nucleic acid molecules (N) and proteins (P), where the
XX proteins are collectively known as colon cancer antigens. The colon
XX cancer antigens have cytostatic activity and can be used in gene therapy
XX and vaccine production. N and P may be used in the prevention, diagnosis
XX and treatment of diseases associated with inappropriate P expression. For
XX example, N and P may be used to treat disorders associated with decreased
XX expression by rectifying mutations or deletions in a patient's genome
XX that affect the activity of P by expressing inactive proteins or to
XX supplement the patient's own production of P. Additionally, N may be used
XX to produce the colon cancer-associated P, by inserting the nucleic acids
XX into a host cell and culturing the cell to express the proteins. N and P
XX can be used in the prevention, diagnosis and treatment of colorectal
XX carcinomas and cancers. AAH37196 to AAH37204 and AAG77789 represent
XX sequences used in the exemplification of the present invention. N.B.
XX Pages 666 to 682 and page 7053 of the sequence listing were missing at
XX time of publication, meaning no sequences are present for SEQ ID NO:1027
XX to 1052, 7921 and 7922
XX
XX Sequence 105 BP; 24 A; 36 C; 32 G; 8 T; 0 U; 5 Other;
XX
XX Query Match 9.6%; Score 24.2; DB 4; Length 105;
XX Best Local Similarity 53.7%; Pred. No. 3.2e+03;
XX Matches 44; Conservative 0; Mismatches 38; Indels 0; Gaps 0;

QY 96 CTGCCACGGCTGAGTTTCGGGCTCCAGGTTCCGCTGCGCTGAGGTTTCGAGGCGACA 155
Db 24 CCGCNACGCCCCGACGAGNACCGGTCCGGAATCCCGGTGACCCACGCGNTTTCGCCAA 83
QY 156 CAGCTCGCAGTCGGGCGAGGAG 177
Db 84 CATGCGGGGCGAGGACGGGGG 105
```

RESULT 6
ABT17318/c
ID ABT17318 standard; DNA; 78 BP.
XX AC ABT17318;
XX AC ABT17318;
XX DT 10-APR-2003 (first entry)
XX DE Transcription factor-related array hybridisation probe - SEQ ID NO 145.
XX KW Probe; ss; transcription factor-protein complex; transcription factor;
XX KW drug screening; drug identification; array hybridisation.
XX OS Unidentified.
XX PN WO2002101351-A2.
XX PD 19-DEC-2002.
XX PF 30-MAY-2002; 2002WO-US017408.
XX PR 08-JUN-2001; 2001US-00877243.
XX PR 08-JUN-2001; 2001US-00877403.
XX PR 08-JUN-2001; 2001US-00877705.
XX PR 08-JUN-2001; 2001US-00877738.
XX PR 05-SEP-2001; 2001US-00947274.
XX PA (PANO-) PANOMICS INC.
XX PI Li X;
XX DR WPI; 2003-148829/14.
XX PT Identifying transcription factor-protein complexes, by isolating
XX PT transcription factor complexes from sample based on a specific type of
XX PT factor, and identifying different proteins present in isolated complexes.
XX PS Disclosure; Fig 6; 167pp; English.
XX CC The invention comprises a method for identifying complexes between a
XX CC transcription factor and another protein. The invention also comprises a
XX CC method for isolating DNA probes which bind to activated transcription
XX CC factors. The methods of the invention are useful for identifying
XX CC transcription factor-protein interactions. The methods of the invention
XX CC are also useful for facilitating the screening and identification of new
XX CC drugs, characterising their mechanism of action and screening for adverse
XX CC side effects based on drug's impact expression. The present DNA sequence
XX CC represents a probe used in the method of the invention
XX SQ Sequence 78 BP; 15 A; 27 C; 15 G; 21 T; 0 U; 0 Other;
Query Match 9.4%; Score 23.8; DB 8; Length 78;
Best Local Similarity 59.7%; Pred. No. 3.9e+03;
Matches 40; Conservative 0; Mismatches 27; Indels 0; Gaps 0;
QY 109 AGTTTCGGCTCCAGGTTCCGCTGTCGCTGAGGTTTGGCCAGACAGCTCGCAGTCG 168
DB 78 AGCTTCAGGTCAGAGGTTCAGAGAGTAGCTTCAGGTCAGAGGTCAGAGAGCTAGTTTCAG 19
QY 169 GGCAGGG 175
DB 18 GTCAGAG 12
RESULT 7
AAC10990/c
ID AAC10990 standard; cDNA; 72 BP.
XX AC AAC10990;
XX DT 06-OCT-2000 (first entry)
XX DE Human secreted protein 5' EST, SEQ ID NO: 15065.
XX KW

XX KW Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;
XX KW gene therapy; chromosome mapping; ss.
XX OS Homo sapiens.
XX PN EP1033401-A2.
XX PD 06-SEP-2000.
XX PF 21-FEB-2000; 2000EP-00200610.
XX PR 26-FEB-1999; 99US-0122487P.
XX PA (GEST) GENSET.
XX PI Dumas Milne Edwards J, Duclert A, Giordano J;
XX DR WPI; 2000-500381/45.
XX PT New nucleic acid that is a 5' expressed sequence tag (5' EST) for
XX PT obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for
XX PT diagnostic, forensic, gene therapy and chromosome mapping procedures.
XX PS Claim 1; SEQ ID NO 15065; 71pp + Sequence Listing; English.
XX CC The present sequence is one of a large number of 5' ESTs derived from
XX CC mRNAs encoding secreted proteins. No ORF has yet been conclusively
XX CC identified within the present sequence. The 5' ESTs were prepared from
XX CC total human RNAs or polyA+ RNAs derived from 30 different tissues. EST
XX CC sequences usually correspond mainly to the 3' untranslated region (UTR)
XX CC of the mRNA because they are often obtained from oligo-dT primed cDNA
XX CC libraries. Such ESTs are not well suited for isolating cDNA sequences
XX CC derived from the 5' ends of mRNAs and even in those cases where longer
XX CC cDNA sequences have been obtained, the full 5' UTR is rarely included. 5'
XX CC ESTs are derived from mRNAs with intact 5' ends and can therefore be used
XX CC to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used in
XX CC diagnostic, forensic, gene therapy and chromosome mapping procedures.
XX CC They are used to obtain upstream regulatory sequences and to design
XX CC expression and secretion vectors
XX SQ Sequence 72 BP; 9 A; 33 C; 20 G; 10 T; 0 U; 0 Other;
Query Match 9.4%; Score 23.6; DB 3; Length 72;
Best Local Similarity 69.6%; Pred. No. 4.4e+03;
Matches 32; Conservative 0; Mismatches 14; Indels 0; Gaps 0;
QY 128 GCGTCTCGCCCTGAGGTTTGGCCAGACAGCTCGCAGTCGGGCGAG 173
DB 58 GCGTGGGGCCCGGGGATCGAGGGCATCCAGCAGAGCGCGCCAG 13
RESULT 8
AAH68919
ID AAH68919 standard; cDNA; 97 BP.
XX AC AAH68919;
XX DT 19-SEP-2001 (first entry)
XX DE Human cervical cancer marker nucleic acid 193.
XX KW Cervical cancer; cytostatic; pre-malignant condition; gene therapy; ss.
XX OS Homo sapiens.
XX PN WO200142467-A2.
XX PD 14-JUN-2001.
XX PF 08-DEC-2000; 2000WO-US033312.
XX PR 08-DEC-1999; 99US-0169681P.
XX PR

```
PR 21-DEC-1999; 99US-0171350P.
PR 14-MAR-2000; 2000US-0189315P.
PR 12-MAY-2000; 2000US-0203791P.
PR 09-JUN-2000; 2000US-0210600P.
PR 21-JUL-2000; 2000US-0220114P.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
XX Schlegel R, Deeds J, Berger A, Zhao X;
XX WPI; 2001-375006/39.
XX New isolated nucleic acid for diagnosing and treating cervical cancer and
PT for assessing and detecting compounds for treating the cancer.
XX Claim 1; Page 137; 1051pp; English.
XX The invention relates to novel genes (AAH68727-AAH73383) associated with
CC cervical cancer with cytostatic activity. The nucleic acids and encoded
CC polypeptides are useful: to assess if a patient is afflicted with
CC cervical cancer or has a pre-malignant condition; to monitor the
CC progression of cervical cancer or a premalignant condition in a patient;
CC and to select and/or assess the efficacy of a compound or therapy for
CC inhibiting cervical cancer in a patient. The nucleic acids may also be
CC useful for gene therapy
XX
XX Sequence 97 BP; 7 A; 34 C; 30 G; 23 T; 0 U; 3 Other;
Query Match 9.4%; Score 23.6; DB 4; Length 97;
Best Local Similarity 59.4%; Pred. No. 4.8e+03;
Matches 38; Conservative 0; Mismatches 26; Indels 0; Gaps 0;
QY 189 GACGAGCGGCTCTGGGCCCTTAATTGTACTTCGGGCTCGPATGTCTCTCTTCGCGCAC 248
DB 6 GCCGAGGTACCGCGGGGCTGNAGTAGGCTTCGCTTCGGNTTTCTCTTCCTTCGCTAA 65
QY 249 CTCC 252
DB 66 CGCC 69
RESULT 9
ACD69745/C
ID ACD69745 standard; DNA; 100 BP.
XX
XX ACD69745;
XX
XX 18-SEP-2003 (first entry)
XX
XX E. coli K12 MG1655 biochip probe SEQ ID 1015.
XX Biochip; gene expression; gut; diagnostic; detection; probe; ss.
XX Escherichia coli.
XX
XX EP1260592-A1.
XX
XX 27-NOV-2002.
XX
XX 17-MAY-2001; 2001EP-00112179.
XX
XX 17-MAY-2001; 2001EP-00112179.
XX (MWGB-) MWG-BIOTECH AG.
XX
XX Donner H, Drescher B, Huber A, Weber J;
XX WPI; 2003-241155/24.
XX
XX Biochip containing probes complementary with open reading frames in
PT Escherichia coli K12, useful for detecting gene expression and expression
XX patterns.
XX
PS Claim 3; Page 1228; 2004pp; German.
XX
XX This invention describes a novel biochip comprising probe spots, each
CC containing many identical probes. The probes are nucleotide sequences of
CC 30-80 bases, are prepared ex situ from synthetic oligonucleotides and at
CC least one includes a segment of at least 20 bases identical with, or
CC complementary to, a segment of an open reading frame (orf) of Escherichia
CC coli K12. The biochip is used for specific detection of gene expression
CC in K12 and for determining the gene expression pattern, e.g. for
CC diagnostic determination of which E. coli strains are present in the gut,
CC and to determine the effects of e.g. growth media on gene expression. The
CC biochip provides as comprehensive as possible detection of the K12
CC genome, with simultaneous analysis of many different genes with a single
CC device, and comparison of gene expression between K12 and its mutants or
CC other E. coli strains in a single experiment. Apart from qualitative and
CC quantitative information about gene expression, it also allows
CC measurements of population densities for the various strains. The use of
CC synthetic oligonucleotides for preparation of probes allows free
CC variation in probe length and ensures high purity (and thus selectivity,
CC reactivity and reproducibility); also synthetic probes are generally
CC shorter than probes prepared by polymerase chain reaction. ACD68731 to
CC ACD81540 represent oligonucleotide probes used with the biochip described
CC in the invention
XX
XX Sequence 100 BP; 21 A; 29 C; 38 G; 12 T; 0 U; 0 Other;
Query Match 9.3%; Score 23.4; DB 8; Length 100;
Best Local Similarity 63.2%; Pred. No. 5.5e+03;
Matches 36; Conservative 0; Mismatches 21; Indels 0; Gaps 0;
QY 100 CACGGGCTGAGTTTCGGCTCCAGGTTCCGGTGTCCCTGAGTTTGGAGCCAGAC 156
DB 88 CAAGTTCTGCGCGCTGCACCATGTTCCAGTGCCTGCGGGTTTCTGCGCAGCC 32
RESULT 10
ACD76587
ID ACD76587 standard; DNA; 100 BP.
XX
XX ACD76587;
XX
XX 18-SEP-2003 (first entry)
XX
XX E. coli K12 MG1655 biochip probe SEQ ID 7863.
XX
XX Biochip; gene expression; gut; diagnostic; detection; probe; ss.
XX Escherichia coli.
XX
XX EP1260592-A1.
XX
XX 27-NOV-2002.
XX
XX 17-MAY-2001; 2001EP-00112179.
XX
XX 17-MAY-2001; 2001EP-00112179.
XX (MWGB-) MWG-BIOTECH AG.
XX
XX Donner H, Drescher B, Huber A, Weber J;
XX WPI; 2003-241155/24.
XX
XX Biochip containing probes complementary with open reading frames in
PT Escherichia coli K12, useful for detecting gene expression and expression
XX patterns.
XX
PS Claim 3; Page 1228; 2004pp; German.
XX
XX This invention describes a novel biochip comprising probe spots, each
CC containing many identical probes. The probes are nucleotide sequences of
CC 30-80 bases, are prepared ex situ from synthetic oligonucleotides and at
CC least one includes a segment of at least 20 bases identical with, or
```

complementary to, a segment of an open reading frame (orf) of *Escherichia coli* K12. The biochip is used for specific detection of gene expression in K12 and for determining the gene expression pattern, e.g. for diagnostic determination of which *E. coli* strains are present in the gut, and to determine the effects of e.g. growth media on gene expression. The biochip provides as comprehensive as possible detection of the K12 genome, with simultaneous analysis of many different genes with a single device, and comparison of gene expression between K12 and its mutants or other *E. coli* strains in a single experiment. Apart from qualitative and quantitative information about gene expression, it also allows measurements of population densities for the various strains. The use of synthetic oligonucleotides for preparation of probes allows free variation in probe length and ensures high purity (and thus selectivity, reactivity and reproducibility); also synthetic probes are generally shorter than probes prepared by polymerase chain reaction. ACD8731 to ACD81540 represent oligonucleotide probes used with the biochip described in the invention

Sequence 100 BP; 13 A; 35 C; 29 G; 23 T; 0 U; 0 Other;

Query Match 9.3%; Score 23.4; DB 8; Length 100;
Best Local Similarity 63.2%; Pred. No. 5.5e+03;
Matches 36; Conservative 0; Mismatches 21; Indels 0; Gaps 0;

QY 100 CACGGCTGAGTTCCGGCTCCAGGTTCCGCTGTCGCCCTGAGGTTTGAGGCCAGAC 156
DB 43 CAAGTTTCGCCGCGCTGCACCATGTTCGCCAGTGCAGCGCGGTTTCGGCCAGCC 99

RESULT 11
ADR28210
ID ADR28210 standard; DNA; 100 BP.

XX ADR28210;
XX 04-NOV-2004 (first entry)
XX Oligonucleotide Dmeter, SEQ ID 9.

XX 2-amino-4-alkylthio-butyric acid; methionine synthase;
XX cystathionine-gamma-synthase; acylhomoserine sulphydrylase; ss.
XX Synthetic.

XX FR2851255-A1.
XX 20-AUG-2004.

XX 14-MAY-2003; 2003FR-00005768.
XX 18-FEB-2003; 2003FR-00001924.

XX (META-) METABOLIC EXPLORER.

XX Chateau M, Gonzales B, Soucaille PNP;
XX WPI; 2004-618123/60.

XX New strains of microorganisms that produce 2-amino-4-alkylthio-butyric acid, useful for preparing L-methionine, from simple carbon source and a mercaptan or its salt, have modified methionine synthase activity.

XX Example 1; SEQ ID NO 9; 68pp; French.

XX The present invention relates to a novel strain (A) of a microorganism which produces a 2-amino-4-alkylthio-butyric acid (I) by metabolising a simple sugar and a thiol (II), or its salt, and has at least one gene encoding an enzyme with modified methionine synthase (MS) activity. (A) are specifically used for fermentative production of L-methionine, which is produced from a simple carbon source and alkylmercaptan, i.e. synthesis of L-Met is independent of synthesis of cysteine; the methyl mercaptan used is a toxic waste product from the petrochemical industry and synthesis of L-Met occurs in a single step from O-(acetyl or

CC succinyl)-L-homoserine. The enzyme with modified MS activity is either cystathionine-gamma-synthase or an acylhomoserine sulphydrylase, and is modified so that the substrate is reacted with (II) rather than with L-cysteine, to result in preferential conversion of the substrate to (I) or homocysteine. The present sequence was used in an example from the CC invention.

XX Sequence 100 BP; 15 A; 36 C; 25 G; 24 T; 0 U; 0 Other;

Query Match 9.3%; Score 23.4; DB 13; Length 100;
Best Local Similarity 63.2%; Pred. No. 5.5e+03;
Matches 36; Conservative 0; Mismatches 21; Indels 0; Gaps 0;

QY 100 CACGGCTGAGTTCCGGCTCCAGGTTCCGCTGTCGCCCTGAGGTTTGAGGCCAGAC 156
DB 12 CAAGTTTCGCCGCGCTGCACCATGTTCGCCAGTGCAGCGCGGTTTCGGCCAGCC 68

RESULT 12
ADR99734
ID ADR99734 standard; DNA; 100 BP.

XX ADR99734;
XX 02-DEC-2004 (first entry)

XX Nucleic acid Dmeter to generate evolved microorganisms.
XX ss; microorganism evolution; metabolic pathway; metabolite;
XX biotransformation; NADPH-dependent enzyme; nucleic acid metabolism;
XX lipid metabolism; sugar metabolism.

XX Unidentified.

XX WO2004076659-A2.

XX 10-SEP-2004.

XX 17-FEB-2004; 2004WO-PR000354.

XX 18-FEB-2003; 2003FR-00001924.

XX 14-MAY-2003; 2003FR-00005768.

XX 14-MAY-2003; 2003FR-00005769.

XX 06-NOV-2003; 2003FR-00013054.

XX (META-) METABOLIC EXPLORER.

XX Chateau M, Gonzalez B, Meynial-Salles I, Soucaille PNP, Zink O;
XX WPI; 2004-653418/63.

XX New evolved microorganisms with altered metabolic pathways, useful e.g. for production of amino acids, are selected as mutants able to grow on defined media.

XX Disclosure; SEQ ID NO 1; 113pp; French.

XX The invention relates to a method for preparing evolved microorganisms (A) with modified metabolic pathways comprising: (a) genetic modification of a microorganism to inhibit production or consumption of a metabolite when it is grown on a defined medium, thus affecting its ability to grow; (b) growing the modified organism in the defined medium so that evolution can occur, optionally with addition of a co-substrate to allow evolution; and (c) selecting as (A) cells able to grow on the medium, optionally in presence of co-substrate. The evolved microorganisms (A), or evolved proteins (I) expressed by them, are useful in biotransformation processes, especially those involving NADPH-dependent enzymes, particularly synthesis of amino acids (Met, Cys, Thr, Lys or Ile) but also synthesis of nucleic acids or lipids, and metabolism of sugars. (A) provide more efficient production of selected metabolites than parent strains. This sequence represents a nucleic acid molecule used in the method of the invention.

XX


```
SQ Sequence 100 BP; 15 A; 36 C; 25 G; 24 T; 0 U; 0 Other;
Query Match          9.3%; Score 23.4; DB 13; Length 100;
Best Local Similarity 63.2%; Pred. No. 5.5e+03;
Matches 36; Conservative 0; Mismatches 21; Indels 0; Gaps 0;

QY 100 CACGGCTGAGTTTCGGCTCCAGGTTCCGCTGCGCCCTGAGGTTGAGGCCAGAC 156
Db 12 CAAGTTCTGCGCGCTGACCATGTTGCGCAGTGCAGTGCAGGTTTCTGGCCAGCC 68

RESULT 13
AAZ89260/C
ID AAZ89260 standard; DNA; 59 BP.
XX
AC AAZ89260;
XX
DT 09-JUN-2000 (first entry)
XX
DE Human embryonic brain protein PCR primer #5.
XX
KW Human; brain; nerve degeneration; nootropic; neuroprotective;
KW anticonvulsant; antiparkinsonian; antidiabetic; treatment; infarction;
KW Parkinson's disease; Alzheimer's disease; Huntington's disease;
KW muscular hypoplastic lateral sclerosis; diabetic neuropathy; PCR primer;
KW ss.
XX
OS Homo sapiens.
XX
PN WO200007614-A1.
XX
PD 17-FEB-2000.
XX
PF 02-AUG-1999; 99WO-JP004171.
XX
PR 05-AUG-1998; 98JP-00221886.
PR 05-FEB-1999; 99JP-00029164.
XX
PA (SAKA) OTSUKA PHARM CO LTD.
XX
PI Horie M, Hirano H, Kyushiki H, Mitsumoto Y, Mori A, Watanabe A;
XX
XX WPI; 2000-205568/18.
XX
PT New protein isolated from human embryonic brain useful for treating nerve
PT degeneration diseases e.g. Parkinson's diseases and Alzheimer's disease.
XX
PS Example 2; Page 62; 69pp; Japanese.
XX
CC This invention describes a novel human embryonic brain derived protein
CC (I) which has nootropic, neuroprotective, anticonvulsant,
CC antiparkinsonian and antidiabetic activity. (I) is useful for treating
CC nerve degeneration diseases e.g. Parkinson's disease, Alzheimer's
CC disease, muscular hypoplastic lateral sclerosis, Huntington's disease,
CC brain infarction, diabetic neuropathy and traumatic nerve degeneration.
CC AAZ89256-289234 represent PCR primers used in the isolation and
CC amplification of the human brain protein described in the method of the
CC invention
XX
SQ Sequence 59 BP; 9 A; 23 C; 14 G; 13 T; 0 U; 0 Other;
Query Match          9.2%; Score 23.2; DB 3; Length 59;
Best Local Similarity 65.4%; Pred. No. 5.5e+03;
Matches 34; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

QY 159 CTCGAGTCGGCAGGAGGGGGGAGAGAGCAGCGGCTCTGGCCCTTA 210
Db 52 CTGGCAGTCGCTCAGGAGGTCGGAAAGCAGCCAGCTTTAACGGGGCGCATA 1

RESULT 14
AAK44587/c
ID AAK44587 standard; DNA; 101 BP.
XX
AC AAK44587;
XX
DT 05-NOV-2001 (first entry)
XX
DE Human brain expressed single exon probe SEQ ID NO: 18650.
XX
KW Human; brain expressed exon; gene expression analysis; probe; microarray;
KW Alzheimer's disease; multiple sclerosis; schizophrenia; epilepsy; cancer;
KW ss.
XX
OS Homo sapiens.
XX
PN WO200157275-A2.
XX
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```
XX
AC AAK44587;
XX
DT 06-NOV-2001 (first entry)
XX
DE Human bone marrow expressed single exon probe SEQ ID NO: 19144.
XX
KW Human; bone marrow expressed exon; gene expression analysis; probe;
KW microarray; cancer; leukaemia; lymphoma; myeloma; ss.
XX
OS Homo sapiens.
XX
PN WO200157276-A2.
XX
PD 09-AUG-2001.
XX
PF 30-JAN-2001; 2001WO-US000668.
XX
PR 04-FEB-2000; 2000US-0180312P.
PR 26-MAY-2000; 2000US-0207456P.
PR 30-JUN-2000; 2000US-00608408.
PR 03-AUG-2000; 2000US-00632366.
PR 21-SEP-2000; 2000US-0234687P.
PR 27-SEP-2000; 2000US-0236359P.
PR 04-OCT-2000; 2000GB-00024263.
XX
PA (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX
XX WPI; 2001-488900/53.
XX
PT Human genome-derived single exon nucleic acid probes useful for analyzing
PT gene expression in human bone marrow.
XX
PS Example 4; SEQ ID NO 19144; 658pp + Sequence Listing; English.
XX
CC The present invention provides a number of single exon nucleic acid
CC probes which are derived from genomic sequences expressed in the human
CC bone marrow. They can be used to measure gene expression in bone marrow
CC samples, which may enable the improved diagnosis and treatment of cancers
CC such as lymphoma, leukaemia and myeloma. The present sequence is one of
CC the probes of the invention
XX
SQ Sequence 101 BP; 36 A; 22 C; 23 G; 20 T; 0 U; 0 Other;
Query Match          9.2%; Score 23.2; DB 4; Length 101;
Best Local Similarity 61.7%; Pred. No. 6.3e+03;
Matches 37; Conservative 0; Mismatches 23; Indels 0; Gaps 0;

QY 27 GTTAAGGCGTCCCAAGTTGGAAGGCGCTTTCGTTCTGTTCTCGATGCAGAGTCTTC 86
Db 64 GCTGAGTCATAACCTGCTCAAGCAGACTGGGTTTCTGATTCTTGATGCCAGAGTTCTC 5

RESULT 15
AAK18659/c
ID AAK18659 standard; DNA; 101 BP.
XX
AC AAK18659;
XX
DT 05-NOV-2001 (first entry)
XX
DE Human brain expressed single exon probe SEQ ID NO: 18650.
XX
KW Human; brain expressed exon; gene expression analysis; probe; microarray;
KW Alzheimer's disease; multiple sclerosis; schizophrenia; epilepsy; cancer;
KW ss.
XX
OS Homo sapiens.
XX
PN WO200157275-A2.
XX
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PD 09-AUG-2001.
XX
PF 30-JAN-2001; 2001WO-US000667.
XX
XX 04-FEB-2000; 2000US-0180312P.
PR 26-MAY-2000; 2000US-0207456P.
PR 30-JUN-2000; 2000US-00608408.
PR 03-AUG-2000; 2000US-00632366.
PR 21-SEP-2000; 2000US-0234687P.
PR 27-SEP-2000; 2000US-0236359P.
PR 04-OCT-2000; 2000GB-00024263.
XX
XX (MOLE-) MOLECULAR DYNAMICS INC.
XX
XX Penn SG, Hanzel DK, Chen W, Rank DR;
XX
XX WPI; 2001-483446/52.
XX
XX Single exon nucleic acid probes for analyzing gene expression in human
PT brains.
XX
XX Example 4; SEQ ID NO 18650; 650pp + Sequence Listing; English.
XX
XX The present invention provides a number of single exon nucleic acid
CC probes which are derived from genomic sequences expressed in the human
CC brain. They can be used to measure gene expression in brain cell samples,
CC which may enable the diagnosis and improved treatment of nervous system
CC diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia,
CC epilepsy and cancers. The present sequence is one of the probes of the
CC invention
XX
XX Sequence 101 BP; 36 A; 22 C; 23 G; 20 T; 0 U; 0 Other;
SQ
Query Match 9.2%; Score 23.2; DB 4; Length 101;
Best Local Similarity 61.7%; Pred. No. 6.3e+03;
Matches 37; Conservative 0; Mismatches 23; Indels 0; Gaps 0;
QY 27 GTTAAGCGTCCCAAGTTGGAGGGCGTTTCTTCTGTTCTGATGCAGAGTCCTC 86
Db 64 GCTGAGTCATACCTGCTTCAAGCAGACTGGGTTTCTGATTCTGATGGCAGAGTCTC 5

Search completed: October 16, 2006, 13:14:41
Job time : 257 secs

GenCore version 5.1.9
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OM nucleic - nucleic search, using sw model

Run on: October 16, 2006, 13:38:19 ; Search time 2284 Seconds
(without alignments)
6169.734 Million cell updates/sec

Title: US-10-604-726A-8797

Perfect score: 252

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Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 48236798 seqs, 27959665780 residues

Total number of hits satisfying chosen parameters: 1484138

Minimum DB seq length: 0

Maximum DB seq length: 120

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:*

1: gb_est1.*

2: gb_est3.*

3: gb_est4.*

4: gb_est5.*

5: gb_est6.*

6: gb_hic.*

7: gb_est2.*

8: gb_est7.*

9: gb_est8.*

10: gb_est9.*

11: gb_ges1.*

12: gb_ges2.*

13: gb_ges3.*

14: gb_ges4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	29	11.5	100	11	AZ769498
2	27.6	11.0	103	12	CG574657
3	26.2	10.4	82	12	CG535738
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C 5	25.8	10.2	110	13	CL952591
6	25.6	10.2	99	7	AV841732
7	25.6	10.2	103	13	DU408432
C 8	25.6	10.2	117	12	CG255380
C 9	25.2	10.0	103	7	AW800261
C 10	25	9.9	100	10	DV900899
C 11	25	9.9	108	11	AZ697609
C 12	24.8	9.8	89	2	BG718505
13	24.8	9.8	116	12	BZ836170
14	24.8	9.8	120	14	CNS02660
15	24.6	9.8	107	4	CB219192
16	24.6	9.8	119	12	BZ987003
C 17	24.4	9.7	95	2	BF724320
C 18	24.4	9.7	109	10	DV552589
19	24.4	9.7	119	9	DN773586

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	22	24.2	9.6	117	13	DU188381	DU188381	109857418
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	24	24	9.5	100	5	CK005996	CK005996	338217r3c
	25	24	9.5	100	13	CL952595	CL952595	OsIRUA001
C	26	24	9.5	101	4	CD029354	CD029354	mgCW016xK
	27	24	9.5	102	12	CC376448	CC376448	RUHA1521D
C	28	24	9.5	105	5	CK451897	CK451897	907470 MA
	29	24	9.5	116	5	CF741809	CF741809	UT-M-HB0-
C	30	23.8	9.4	93	5	CK100624	CK100624	C057P42_5
	31	23.8	9.4	101	2	BJ965328	BJ965328	BJ965328
	32	23.8	9.4	102	2	BJ965717	BJ965717	BJ965717
	33	23.8	9.4	102	2	BJ970068	BJ970068	BJ970068
	34	23.8	9.4	103	2	BJ967675	BJ967675	BJ967675
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	36	23.8	9.4	109	2	BJ968752	BJ968752	BJ968752
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	41	23.6	9.4	109	7	AW493199	AW493199	UT-M-BH3-
	42	23.6	9.4	113	11	AZ922634	AZ922634	SLCot2D11
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	45	23.4	9.3	106	2	BG994249	BG994249	CM3-HT115

ALIGNMENTS

RESULT 1
AZ769498
LOCUS
DEFINITION
1M0570K16F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0570K16 F, genomic survey sequence.
ACCESSION
AZ769498
VERSION
AZ769498.1 GI:12889695
KEYWORDS
GSS.
SOURCE
Mus musculus (house mouse)
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridea; Muridae; Murinae; Mus.
REFERENCE
1 (bases 1 to 100)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
TITLE
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL
Unpublished (2000)
COMMENT
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddm@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0570 row: K column: 16
Seq primer: CGTTGTAAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 100.

FEATURES

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/mol_type="genomic DNA"
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/db_xref="taxon:10090"
/clone="UUGC1M0570K16"
/sex="Male"

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DU188381 109857418
BZ585533 3590_1_36
CK005996 3382178ic
CL952595 O8IRUA001
CD029354 mgcw016xx
CC376448 FUBA152TD
CF741809 UT-M-HB0-
CK100624 C057P42_5
BJ965328 BJ965328
BJ965717 BJ965717
BJ970068 BJ970068
BJ967675 BJ967675
BJ967592 BJ967592
BJ968752 BJ968752
AW619414 7468 MARC
BJ554385 BJ554385
AJ924324 AJ924324
CB221358 1DU004F03
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AZ922634 SLCC02D11
CN868873 001202AAO
CO018108 EST788490
BG994249 CM3-HT115

/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /notes="Vector: pWD42nv; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adaptor DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of pWD42 [gi|4732114|gb|AF129072.1], a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adaptor mouse DNA was annealed to
 adaptor vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

ORIGIN

Query Match 11.5%; Score 29; DB 11; Length 100;
 Best Local Similarity 71.7%; Pred. No. 3.3e+03;
 Matches 38; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

QY 147 GAGGCAGACAGCTCGCAGTCGGGAGGAGGGGGGAGACAGCGGCT 199
 |||||
 Db 23 GCGGCAGGTGAGCGCTCCGCCGCGGGAGAGCGGGAGAGCGGCT 75
 |||||

RESULT 2

CG574657 103 bp mRNA linear GSS 02-OCT-2003
 LOCUS OST207730 Mus musculus 129Sv/Ev Mus musculus cDNA clone OST207730,
 DEFINITION mRNA sequence.

ACCESSION CG574657.1 GI:37364994
 VERSION
 KEYWORDS
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 103)
 AUTHORS Zambronicz,B.P., Abuin,A., Ramirez-Solis,R., Richter,L.J.,
 Piggett,J., BeltrandelRio,H., Buxton,E.C., Edwards,J., Finch,R.A.,
 Fridde,C.J., Gupta,A., Hansen,G., Hu,Y., Huang,W., Jaing,C.,
 Key,B.W. Jr., Kipp,P., Kohlhauff,B., Ma,Z.-Q., Markesich,D.,
 Payne,R., Potter,D.G., Qian,N., Shaw,J., Schrick,J., Shi,Z.-Z.,
 Sparks,M.J., Van Sligtenhorst,I., Vogel,P., Walke,W., Xu,N.,
 Zhu,Q., Person,C. and Sands,A.T.

FEATURES

source
 1..82
 /organism="Mus musculus"
 /mol_type="mRNA"
 /db_xref="taxon:10090"
 /clone="OST122945"
 /cell_type="embryonic stem cell"
 /clone_lib="Mus musculus 129Sv/Ev"

TITLE

Wnk1 kinase deficiency lowers blood pressure in mice: a gene-trap
 screen to identify potential targets for therapeutic intervention

JOURNAL

PUBMED 14610273
 COMMENT Proc. Natl. Acad. Sci. U.S.A. 100 (24), 14109-14114 (2003)
 Contact: Zambrowicz BP
 OmniBank

Lexicon Genetics Incorporated
 4000 Research Forest Drive, The Woodlands, TX 77381, USA
 Email: materials@lexgen.com
 Gene trap sequence tag generated by 3' RACE from mouse ES cells as
 described in Zambrowicz et al (Nature. 1998 Apr 9;392(6676):608-11)

CLASS

Gene Trap.

Location/Qualifiers

1..103
 /organism="Mus musculus"
 /mol_type="mRNA"
 /strain="129Sv/Ev"
 /db_xref="taxon:10090"
 /clone="OST207730"
 /cell_type="embryonic stem cell"

FEATURES

source

1..103

/organism="Mus musculus"
 /mol_type="mRNA"
 /strain="129Sv/Ev"
 /db_xref="taxon:10090"
 /clone="OST207730"
 /cell_type="embryonic stem cell"

ORIGIN

Query Match 11.0%; Score 27.6; DB 12; Length 103;
 Best Local Similarity 67.2%; Pred. No. 8e+03;
 Matches 39; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

QY 39 CCAAGTTGAAGGGCGCTTGTCTCTGTTTCTGGATGACAGATCCTCTGACTCCCTC 96
 |||||
 Db 42 CCACCTTGATAGACACTCTGAGGTTCTTTCTGGATCAAGCGTCTTACTGCTTC 99
 |||||

RESULT 3

CG535738 82 bp mRNA linear GSS 01-OCT-2003
 LOCUS OST122945 Mus musculus 129Sv/Ev Mus musculus cDNA clone OST122945,
 DEFINITION mRNA sequence.

ACCESSION CG535738
 VERSION
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 82)
 AUTHORS Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
 Sciurognathi; Muridea; Muridae; Murinae; Mus.
 Zambronicz,B.P., Abuin,A., Ramirez-Solis,R., Richter,L.J.,
 Piggett,J., BeltrandelRio,H., Buxton,E.C., Edwards,J., Finch,R.A.,
 Fridde,C.J., Gupta,A., Hansen,G., Hu,Y., Huang,W., Jaing,C.,
 Key,B.W. Jr., Kipp,P., Kohlhauff,B., Ma,Z.-Q., Markesich,D.,
 Payne,R., Potter,D.G., Qian,N., Shaw,J., Schrick,J., Shi,Z.-Z.,
 Sparks,M.J., Van Sligtenhorst,I., Vogel,P., Walke,W., Xu,N.,
 Zhu,Q., Person,C. and Sands,A.T.

TITLE

Wnk1 kinase deficiency lowers blood pressure in mice: a gene-trap
 screen to identify potential targets for therapeutic intervention

JOURNAL

PUBMED 14610273
 COMMENT Proc. Natl. Acad. Sci. U.S.A. 100 (24), 14109-14114 (2003)
 Contact: Zambrowicz BP
 OmniBank

Lexicon Genetics Incorporated
 4000 Research Forest Drive, The Woodlands, TX 77381, USA
 Email: materials@lexgen.com
 Gene trap sequence tag generated by 3' RACE from mouse ES cells as
 described in Zambrowicz et al (Nature. 1998 Apr 9;392(6676):608-11)

CLASS

Gene Trap.

Location/Qualifiers

1..82
 /organism="Mus musculus"
 /mol_type="mRNA"
 /strain="129Sv/Ev"
 /db_xref="taxon:10090"
 /clone="OST122945"
 /cell_type="embryonic stem cell"
 /clone_lib="Mus musculus 129Sv/Ev"

TITLE

Wnk1 kinase deficiency lowers blood pressure in mice: a gene-trap
 screen to identify potential targets for therapeutic intervention

JOURNAL

PUBMED 14610273

COMMENT Proc. Natl. Acad. Sci. U.S.A. 100 (24), 14109-14114 (2003)

Contact: Zambrowicz BP

OmniBank

Lexicon Genetics Incorporated

4000 Research Forest Drive, The Woodlands, TX 77381, USA

Email: materials@lexgen.com

Gene trap sequence tag generated by 3' RACE from mouse ES cells as

described in Zambrowicz et al (Nature. 1998 Apr 9;392(6676):608-11)

Class: Gene Trap.

Location/Qualifiers

1..82

/organism="Mus musculus"

/mol_type="mRNA"

/strain="129Sv/Ev"

/db_xref="taxon:10090"

/clone="OST122945"

/cell_type="embryonic stem cell"

/clone_lib="Mus musculus 129Sv/Ev"

Query Match 10.4%; Score 26.2; DB 12; Length 82;

Best Local Similarity 56.6%; Pred. No. 1.9e+04;

Matches 43; Conservative 0; Mismatches 33; Indels 0; Gaps 0;

QY 64 TGTTCCTGGATGACAGTCTCTGACTCCCTCTGCCACGGGCTGAGTTCCGGCTCCAG 123

|||||

Db 6 TGTTCCTGGATGACAGTCTCTGACTCCCTCTGCCACGGGCTGAGTTCCGGCTCCAG 123

|||||

QY 124 GTTCGGGTGTCGCCCT 139

|||||

Db 66 CTTGATATGAGGCCCT 81

|||||

RESULT 4

CK014560/c

LOCUS CK014560

DEFINITION 33148rsicel_6492.y1 Oryza sativa cv. PA64s panicle sterile cDNA

EST 04-FEB-2005

linear mRNA

110 bp

PA64s panicle sterile cDNA

library *Oryza sativa* (indica cultivar-group) cDNA 5', mRNA sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

CK014560
GI:58604032
EST.

Oryza sativa (indica cultivar-group)
Oryza sativa (indica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzaceae; *Oryza*.

REFERENCE
AUTHORS

Yu, J., Wang, J., Lin, W., Li, S., Li, H., Zhou, J., Ni, P., Dong, W.,
Hu, S., Zeng, C., Zhang, J., Zhang, Y., Li, R., Xu, Z., Li, S., Li, X.,
Zheng, H., Cong, L., Lin, L., Yin, J., Geng, J., Li, G., Shi, J., Liu, J.,
Lv, H., Li, J., Wang, J., Deng, Y., Ran, L., Shi, X., Wang, X., Wu, Q.,
Li, C., Ren, X., Wang, J., Wang, X., Li, D., Liu, D., Zhang, X., Ji, Z.,
Zhao, W., Sun, Y., Zhang, Z., Bao, J., Han, Y., Dong, L., Ji, J., Chen, P.,
Wu, S., and Liu, J.

The Genomes of *Oryza sativa*: A History of Duplications
PLOS Biol. 3 (2), e38 (2005)

TITLE
JOURNAL
PubMed

15685292
Contact: Yan Zhou
Bioinformatics Department
Hangzhou Genomics Institute
No.51 Zhijiang Road, Hangzhou 310008, China

Tel: 86-571-56805886

Fax: 86-571-56805886

Email: zhouyan@genomics.org.cn

Seq primer: M13 Forward

High quality sequence stop: 110

POLYA=No.

FEATURES
source

1..110
Location/Qualifiers

/organism="Oryza sativa (indica cultivar-group)"

/mol_type="mRNA"

/cultivar="PA64s"

/db_xref="taxon:39946"

/tissue_type="panicle"

/cell_type="sterile"

/dev_stage="heading/flowering"

/clone_lib="Oryza sativa cv. PA64s panicle sterile cDNA library"

ORIGIN

Query Match

Best Local Similarity 10.2%; Score 25.8; DB 5; Length 110;

Mismatches 0; Mismatches 27; Indels 0; Gaps 0;

QY 127 CGCGTGTCCCTGAGTTTGAGCGGCAGACAGCTCGCAGTCGGCGAGGCGGGGGA 186

Db 77 CGCCAGCCCGCTTCAGCTTGAGGCGCCACATGCGCGGAGATGGGGAGGA 18

QY 187 GAGACGAGC 195

Db 17 GAGAGAAGC 9

RESULT 5
CL952591/c

LOCUS
DEFINITION
OSIRUA001748 *Oryza sativa* Express Library *Oryza sativa* (indica
cultivar-group) genomic, genomic survey sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

CL952591
GI:52364600
GSS.

Oryza sativa (indica cultivar-group)

Oryza sativa (indica cultivar-group)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzaceae; *Oryza*.

REFERENCE
AUTHORS

1 (bases 1 to 110)
Ma, L., Wang, J., Chen, C., Liu, X., Su, N., Li, L., Wang, X., Cao, M.,
Jiao, Y., Sun, N., Zhang, X., Bao, J., Sun, D., Zhao, H., Yuan, L.,

TITLE

JOURNAL
COMMENT

Wong, G.K.S., Deng, X.W. and Wang, J.
An analysis of transcriptional regulation of the rice genome and
its comparison to Arabidopsis
Unpublished (2004)

Contact: Chen Chen

Department of Bioinformatic

Beijing Institute of Genomics

Chinese Academy of Sciences, Beijing 101300, China

Tel: 86-10-80481559

Fax: 86-10-80486676

Email: chenchen@genomics.org.cn

Rice genomic sequence.

Class: exon-trapped.

FEATURES
source

1..110
Location/Qualifiers

/organism="Oryza sativa (indica cultivar-group)"

/mol_type="genomic DNA"

/db_xref="taxon:39946"

/clone_lib="Oryza sativa Express Library"

/note="Oryza sativa exon trapped genomic sequences"

ORIGIN

Query Match

Best Local Similarity 10.2%; Score 25.8; DB 13; Length 110;

Mismatches 42; Conservative 0; Mismatches 27; Indels 0; Gaps 0;

QY 127 CGCGTGTCCCTGAGTTTGAGCGGCAGACAGCTCGCAGTCGGCGAGGCGGGGGA 186

Db 77 CGCCAGCCCGCTTCAGCTTGAGGCGCCACATGCGCGGAGATGGGGAGGA 18

QY 187 GAGACGAGC 195

Db 17 GAGAGAAGC 9

RESULT 6
AV841732

LOCUS

DEFINITION

AV841732 Nori Satoh unpublished cDNA library, egg Ciona

intestinalis cDNA clone rcieg05m22, mRNA sequence.

ACCESSION

VERSION

AV841732.1 GI:16785883

KEYWORDS

SOURCE

ORGANISM

Ciona intestinalis

Ciona intestinalis

Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;

Phlebobranchia; Cionidae; Ciona.

REFERENCE

AUTHORS

Expressed genes in Ciona intestinalis

Unpublished (2000)

JOURNAL

COMMENT

Contact: Nori Satoh

Department of Zoology

Kyoto University

Sakyo-ku, Kyoto, Kyoto 606-8502, Japan

Tel: 81-75-753-4081

Fax: 81-75-705-1113

Email: satoheascidian.zool.kyoto-u.ac.jp.

Location/Qualifiers

1..99

/organism="Ciona intestinalis"

/mol_type="mRNA"

/db_xref="taxon:7719"

/clone="rcieg05m22"

/tissue_type="whole animal"

/dev_stage="egg"

/clone_lib="Nori Satoh unpublished cDNA library, egg"

ORIGIN

Query Match

Best Local Similarity 10.2%; Score 25.6; DB 7; Length 99;

Mismatches 37; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

```

QY      8  CTGCAACTGAGGGGCTGTTAAGCGCTCCCAAGTTCGAGGGGGCTTTTGCTTC 63
Db      16  CTTGCTGTAAGTGGGTTGAATGGGTTTCCCAACATTTGAGGTGACATTGCTTC 71

RESULT 7
DU408432          103 bp  DNA  linear  GSS 05-OCT-2005
LOCUS            1098474026684 CHORI-243 Ovis aries genomic clone CH243-202P18,
DEFINITION      genomic survey sequence.
ACCESSION       DU408432
VERSION         DU408432.1 GI:77138562
KEYWORDS        GSS.
SOURCE          Ovis aries (sheep)
ORGANISM        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                  Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
                  Pecora; Bovidae; Caprinae; Ovis.
REFERENCE       1  (bases 1 to 103)
AUTHORS        Kirkness,E., Shetty,J., de Jong,P., McEwan,J.C., Oddy,H. and
                  Cockett,N.
TITLE          Ovine BAC End Sequences from Library CHORI-243
JOURNAL
COMMENT        Other GSSs: 1098474028028
                  Contact: Ewen Kirkness
                  The Institute for Genomic Research (TIGR: www.tigr.org)
                  9712 Medical Center Drive, Rockville, MD 20850, USA
                  Tel: 301-795-7536
                  Email: ekirknes@tigr.org
                  Sequences generated at The J. Craig Venter Institute Joint
                  Technology Center (JCVI/JTC; http://www.venterlinstitute.org/).
                  Original Trace: 1098474026684 Trace TI: gnl[ti]918952333
                  Insert Length: 184000 Std Error: 0.00 row: P column: 18
                  Seq primer: SP6
                  Classes: BAC ends.
FEATURES        Location/Qualifiers
source          1..103
                  /organism="Ovis aries"
                  /mol_type="genomic DNA"
                  /strain="Texel breed"
                  /db_xref="taxon:9940"
                  /clone="CH243-202P18"
                  /sex="Male"
                  /cell_type="Blood"
                  /clone_lib="CHORI-243"
                  /notes="vector: pTARBAC2.1; Site_1: EcoRI; Site_2: EcoRI;
                  The CHORI-243 sheep (M) (Ovis aries) BAC library produced
                  by Pieter de Jong's lab at CHORI
                  http://bacpac.chori.org/library.php?id=162"
ORIGIN
Query Match      10.2%; Score 25.6; DB 13; Length 103;
Best Local Similarity 55.7%; Pred. No. 2.9e+04;
Matches 49; Conservative 0; Mismatches 39; Indels 0; Gaps 0;

QY      64  TGTGTTTCGATGCAGAGTCCCTGACTCCCTGCGACGGGCTGAGTTTCGGGCTCCAG 123
Db      4  TGTGTTCAAATGCAGAAATCAGAAATGTACATTTCCAGTCTCGGTGACGGGCCCCG 63

QY      124  GTTCGGGTGTGCGCCCTCGAGGTTTGAGGC 151
Db      64  GGTGGGGGGGAGGCTGGGGGTGAGGC 91

RESULT 8
CG255380/c
LOCUS            CG255380 117 bp  DNA  linear  GSS 25-AUG-2003
DEFINITION      OGVCEP2H2M_0.7_1.5_KB Zea mays genomic clone ZMMBMA0505P16,
                  genomic survey sequence.
ACCESSION       CG255380
VERSION         CG255380.1 GI:34159750
KEYWORDS        GSS.
SOURCE          Zea mays
ORGANISM        Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
                  Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
                  clade; Panicoideae; Andropogoneae; Zea.
REFERENCE       1  (bases 1 to 117)
AUTHORS        Whitelaw,C.A., Quackenbush,J., Van Aken,S., Utterback,T.,
                  Resnick,A., Fraser,C.M., Budiman,M.A., Bedell,J.A., Rohlfing,T.,
                  Citek,R.W., Nunberg,A., Robbins,D. and Lakey,N.
TITLE          Consortium for Maize Genomics
JOURNAL
COMMENT        Unpublished (2002)
                  Contact: Cathy Whitelaw
                  TIGR
                  9712 Medical Center Drive, Rockville, MD 20850, USA
                  Tel: 301-838-5843
                  Fax: 301-838-0208
                  Email: whitelaw@tigr.org
                  Seq primer: TR
                  Class: methylation filtered.
FEATURES        Location/Qualifiers
source          1..117
                  /organism="Zea mays"
                  /mol_type="genomic DNA"
                  /strain="B73"
                  /db_xref="taxon:4577"
                  /clone="ZMMBMA0505P16"
                  /clone_lib="ZM 0.7 1.5 KB"
                  /note="Vector: pBCSK; Site 1: HincII; 0.7-1.5 kb
                  methylation filtered genomic DNA library"
ORIGIN
Query Match      10.2%; Score 25.6; DB 12; Length 117;
Best Local Similarity 57.5%; Pred. No. 2.9e+04;
Matches 46; Conservative 0; Mismatches 34; Indels 0; Gaps 0;

QY      128  GCGTGTCCGCTGAGGTTTGAGGCCAGACAGCTCCAGTCGGCGAGGAGCGGGGAG 187
Db      104  GCGGTCCGGCCAGCGATGTGAAGCACGGCCGACATCTCGGTCTCGGGGGCGGCCAG 45

QY      188  AGACGAGCGGCTCTGCGCCCC 207
Db      44  CGATGTGAAGCTCCGGCCTC 25

RESULT 9
AW800261/c
LOCUS            AW800261 103 bp  mRNA  linear  EST 16-MAY-2000
DEFINITION      MR2-UM0060-170400-203-e06 UM0060 Homo sapiens cDNA, mRNA sequence.
ACCESSION       AW800261
VERSION         AW800261.1 GI:7852131
KEYWORDS        EST.
SOURCE          Homo sapiens (human)
ORGANISM        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                  Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                  Hominidae; Homo.
REFERENCE       1  (bases 1 to 103)
AUTHORS        Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
                  Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.P.,
                  Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
                  Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V.,
                  O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
                  Simpson,A.J.
TITLE          Shotgun sequencing of the human transcriptome with ORF expressed
                  sequence tags
JOURNAL
PUBMED          Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
COMMENT        Contact: Simpson A.J.G.
                  Laboratory of Cancer Genetics
                  Ludwig Institute for Cancer Research
                  Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                  Brazil
                  Tel: +55-11-2704922
                  Fax: +55-11-2707001

```

ORIGIN

```

Query Match          9.9%; Score 25; DB 11; Length 108;
Best Local Similarity 69.4%; Pred. No. 4.2e+04;
Matches 34; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

QY 59 GCTTCTGTTTCTGATGCAGAGTCTCTGACTCTCTGACCGCGGCT 107
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 90 GCTTCTTCTTACTCTGCGCAGAGGCTCAGGCTCTCTTCACGCGGCT 42

RESULT 12
BG718505/c
LOCUS          89 bp      mRNA      linear      EST 08-MAY-2001
DEFINITION    602696562F1 NIH_MGC_97 Homo sapiens cDNA clone IMAGE:4828574 5',
              mRNA sequence.
ACCESSION     BG718505
VERSION       BG718505.1 GI:13997692
KEYWORDS      EST.
SOURCE        Homo sapiens (human)
ORGANISM      Homo sapiens
              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
              Homnidae; Homo.
REFERENCE     1 (bases 1 to 89)
              NIH-MGC http://mgi.nci.nih.gov/.
AUTHORS      National Institutes of Health, Mammalian Gene Collection (MGC)
TITLE        Unpublished (1999)
JOURNAL      Contact: Robert Strausberg, Ph.D.
              Email: cgabs-k@mail.nih.gov
COMMENT      Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
              cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki
              Toshiyuki and Piero Carninci (RIKEN)
              cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
              DNA Sequencing by: Incyte Genomics, Inc.
              Clone distribution: MGC clone distribution information can be
              found through the I.M.A.G.E. Consortium/LLNL at:
              http://image.llnl.gov
              Plate: LLAM10746 row: 1 column: 15
              High quality sequence stop: 19.
FEATURES      Location/Qualifiers
              1..89
                 /organism="Homo sapiens"
                 /mol_type="mRNA"
                 /db_xref="taxon:9606"
                 /clone="IMAGE:4828574"
                 /lab_host="DH10B"
                 /clone_lib="NIH_MGC_97"
                 /notes="Organ: testis; Vector: pBluescriptR (modified
                 pBluescript KS+); Site 1: BamHI; Site 2: SalI-XhoI
                 (gtcgag); Oligo-dT primed using primer
                 5'-TTTTTTTTTTTNN-3', size-selected for average
                 insert size 2.2 kb and normalized to ROT 5. This is a
                 primary library enriched for full-length clones and
                 constructed using the Cap-trapper method (Carninci, in
                 preparation). Library constructed by M. Brownstein
                 (NIH/NHGRI, National Institutes of Health). Note: this is
                 a NIH_MGC Library."
ORIGIN
Query Match          9.8%; Score 24.8; DB 2; Length 89;
Best Local Similarity 57.9%; Pred. No. 4.7e+04;
Matches 44; Conservative 0; Mismatches 32; Indels 0; Gaps 0;

QY 124 GTTCGGGTGTCGCCCTCAGGTTTGAGCCAGACAGCTCGCAGTCGGGAGGCGGG 183
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 76 GTGAGTGGGGTGCTCTGTGGTTGGGGCGGTGTGCTCCCTGGGCCGGGAGCGCG 17

QY 184 GGAGACACGACCGCT 199
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 16 GCGAGGGTAGCCGCT 1

RESULT 13
BZ836170
LOCUS          116 bp      DNA      linear      GSS 18-MAR-2003
DEFINITION    CH240_225C14.TJ CHORI-240 Bos taurus genomic clone CH240_225C14,
              genomic survey sequence.
ACCESSION     BZ836170
VERSION       BZ836170.1 GI:29063528
KEYWORDS      GSS.
SOURCE        Bos taurus (cattle)
ORGANISM      Bos taurus
              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
              Pecora; Bovidae; Bovinae; Bos.
REFERENCE     1 (bases 1 to 116)
              Zhao, S., Shetty, J., Shatsman, S., Tsegaye, G., Geer, K.,
              Shvartsbeyn, A., Gebregeorgis, E., Chen, D., Riggs, F., de Jong, P.,
              Crawford, A. M. and McEwan, J. C. Library CHORI-240
              Bovine BAC End Sequences from
              Unpublished (2003)
              Contact: Shaying Zhao
              Department of Eukaryotic Genomics
              The Institute for Genomic Research
              9712 Medical Center Dr., Rockville, MD 20850, USA
              Tel: 301 838 0200
              Fax: 301 838 0208
              Email: szhao@tigr.org
              Clones are derived from the bovine BAC library CHORI-240
              (http://www.chori.org/bacpac/bovine240.htm). For BAC library
              availability, please contact Pieter de Jong (pdejong@mail.cho.org).
              Clones may be purchased from BACPAC Resources
              (http://www.chori.org/bacpac/ordering_information.htm). This work
              was undertaken as part of the International Bovine BAC Mapping
              Consortium (IBBMC) by AgResearch Ltd., New Zealand and The
              Institute of Genomic Research (TIGR), USA.
              Plate: 225 row: C column: 14
              Seq primer: SP6
              Class: BAC ends.
FEATURES      Location/Qualifiers
              1..116
                 /organism="Bos taurus"
                 /mol_type="genomic DNA"
                 /strain="breed: Hereford"
                 /db_xref="taxon:9913"
                 /clone="CH240_225C14"
                 /sex="Male"
                 /cell_type="Blood"
                 /clone_lib="CHORI-240"
                 /note="Vector: pTARBAC1.3; Site 1: MboI; Site 2: MboI;
                 Hereford bull LI Domino 99375; CHORI-240 Bovine BAC
                 library (Male) produced by Pieter de Jong"
ORIGIN
Query Match          9.8%; Score 24.8; DB 12; Length 116;
Best Local Similarity 63.3%; Pred. No. 4.9e+04;
Matches 38; Conservative 0; Mismatches 22; Indels 0; Gaps 0;

QY 140 GAGGTTTGAGGCGACAGCTCGCAGTCGGGAGGCGGCGGAGAGACGAGCGGT 199
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 36 GAGATATGAGACCAAGTACCCGGGGAGGGGAGGGGCTGCGAGAGAGAGGAT 95

RESULT 14
CNS02660
LOCUS          120 bp      DNA      linear      GSS 01-SEP-2000
DEFINITION    Tetraodon nigroviridis genome survey sequence PUC-Ori end of clone
              240C22 of library G from Tetraodon nigroviridis, genomic survey
              sequence.
ACCESSION     AL182961
VERSION       AL182961.1 GI:7821065
KEYWORDS      GSS; genome survey sequence.
SOURCE        Tetraodon nigroviridis
              Tetraodon nigroviridis
              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
              Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;

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RESULT 2
US-09-210-305C-1
; Sequence 1, Application US/09210305C
; Patent No. 6651010
; GENERAL INFORMATION:
; APPLICANT: Inha University Foundation
; TITLE OF INVENTION: A vector-based method for
; visualizing secondary structure of RNA molecules
;
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BACHMAN & LAPOINTE, P.C.
; STREET: Suite 1201, 900 Chapel Street
; CITY: New Haven
; STATE: Connecticut
;

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;
; COUNTRY: U.S.A.
; ZIP: 06510-2802
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 1.44 Mb storage
; COMPUTER: IBM
; OPERATING SYSTEM: WINDOWS 95/98
; SOFTWARE: MS WORD
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/210,305C
; FILING DATE: 11-Dec-1998
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 96 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: oligonucleotide
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-210-305C-1

Query Match          9.6%; Score 24.2; DB 3; Length 96;
Best Local Similarity 43.5%; Pred. No. 5.6e+02;
Matches 30; Conservative 11; Mismatches 28; Indels 0; Gaps 0;

QY 32 GCGTCCCAAGTTGGAAGGCGCTTGTCTGTTTCTGATGCAGAGTCCTCTGACT 91
Db 10 GCGCGCUGCAAGUCGAAUUGCGCUGUCUGUCGCGCCUGGUGGACUGGCCU 69

QY 92 CCTCTGCC 100
Db 70 GCUUGGCC 78

RESULT 3
US-09-877-243A-145/c
; Sequence 145, Application US/09877243A
; Patent No. 6696256
; GENERAL INFORMATION:
; APPLICANT: Li, Jason
; TITLE OF INVENTION: METHOD AND KIT FOR ISOLATING DNA PROBES THAT BIND TO ACTIVATED
; FILE OF INVENTION: TRANSCRIPTION FACTORS
; FILE REFERENCE: 26757-702
; CURRENT APPLICATION NUMBER: US/09/877,243A
; CURRENT FILING DATE: 2001-08-16
; NUMBER OF SEQ ID NOS: 162
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 145
; LENGTH: 78
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Hybridization probe MP74
US-09-877-243A-145

Query Match          9.4%; Score 23.8; DB 3; Length 78;
Best Local Similarity 59.7%; Pred. No. 7e+02;
Matches 40; Conservative 0; Mismatches 27; Indels 0; Gaps 0;

QY 109 AGTTTCCGGCTCCAGGTTCCGCTGTCGCCCTCGAGGTTTGAGGCCAGACAGCTCGCAGTCG 168
Db 78 AGCTTCAGGTCAGAGGTCAGAGAGTAGCTTCAGGTCAGAGGTCAGAGAGCTAGCTTCAG 19

QY 169 GGCAGGG 175
Db 18 GTCAGAG 12

RESULT 4
US-09-877-705A-145/c
; Sequence 145, Application US/09877705A
; Patent No. 6821737
; GENERAL INFORMATION:
; APPLICANT: Li, Jason
; TITLE OF INVENTION: METHOD AND KIT FOR ISOLATING DNA PROBES THAT BIND TO ACTIVATED
; FILE OF INVENTION: TRANSCRIPTION FACTORS
; FILE REFERENCE: 26757-701
; CURRENT APPLICATION NUMBER: US/09/877,738C
; CURRENT FILING DATE: 2001-08-08
; NUMBER OF SEQ ID NOS: 162
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 145
; LENGTH: 78
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Hybridization probe MP74
US-09-877-738C-145

Query Match          9.4%; Score 23.8; DB 3; Length 78;
Best Local Similarity 59.7%; Pred. No. 7e+02;
Matches 40; Conservative 0; Mismatches 27; Indels 0; Gaps 0;

QY 109 AGTTTCCGGCTCCAGGTTCCGCTGTCGCCCTCGAGGTTTGAGGCCAGACAGCTCGCAGTCG 168
Db 78 AGCTTCAGGTCAGAGGTCAGAGAGTAGCTTCAGGTCAGAGGTCAGAGAGCTAGCTTCAG 19

QY 169 GGCAGGG 175
Db 18 GTCAGAG 12

RESULT 5
US-09-877-738C-145/c
; Sequence 145, Application US/09877738C
; Patent No. 6924113
; GENERAL INFORMATION:
; APPLICANT: Li, Jason
; TITLE OF INVENTION: METHOD AND KIT FOR ISOLATING DNA PROBES THAT BIND TO ACTIVATED
; FILE OF INVENTION: TRANSCRIPTION FACTORS
; FILE REFERENCE: 26757-701
; CURRENT APPLICATION NUMBER: US/09/877,738C
; CURRENT FILING DATE: 2001-08-08
; NUMBER OF SEQ ID NOS: 162
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 145
; LENGTH: 78
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Hybridization probe MP74
US-09-877-738C-145

Query Match          9.4%; Score 23.8; DB 3; Length 78;
Best Local Similarity 59.7%; Pred. No. 7e+02;
Matches 40; Conservative 0; Mismatches 27; Indels 0; Gaps 0;

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Db 78 AGCTTCAGGTCAGAGGTCAGAGAGTAGCTTCAGGTCAGAGGTCAGAGAGCTAGCTTCAG 19

QY 169 GGCAGGG 175
Db 18 GTCAGAG 12

RESULT 6
US-09-513-999C-15065/c
; Sequence 15065, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; Patent No. 6783961
; FILE REFERENCE: 59.US2.REG
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; TITLE OF INVENTION: METHOD FOR SCREENING FOR DRUG CANDIDATES FOR MODULATING TRANSCRIPT1
; TITLE OF INVENTION: FACTOR ACTIVITY
; FILE REFERENCE: 26757-704
; CURRENT APPLICATION NUMBER: US/09/877,705A
; CURRENT FILING DATE: 2001-08-16
; NUMBER OF SEQ ID NOS: 162
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 145
; LENGTH: 78
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Hybridization probe MP74
US-09-877-705A-145

Query Match          9.4%; Score 23.8; DB 3; Length 78;
Best Local Similarity 59.7%; Pred. No. 7e+02;
Matches 40; Conservative 0; Mismatches 27; Indels 0; Gaps 0;

QY 109 AGTTTCCGGCTCCAGGTTCCGCTGTCGCCCTCGAGGTTTGAGGCCAGACAGCTCGCAGTCG 168
Db 78 AGCTTCAGGTCAGAGGTCAGAGAGTAGCTTCAGGTCAGAGGTCAGAGAGCTAGCTTCAG 19

QY 169 GGCAGGG 175
Db 18 GTCAGAG 12
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86 CTGACTCCCTCTGACACGGGCTGAGTTTCGGCTCCAGGTTCCGGTGTGCGCC 138

US-09-347-613C-13/c

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; Sequence 13, Application US/09347613C
; Patent No. 6593133
; GENERAL INFORMATION:
; APPLICANT: Johansen, Teit E.
; APPLICANT: Blom, Nikolaj
; APPLICANT: Hansen, Claus
; TITLE OF INVENTION: No. 6593133el Neurotrophic Factors
; FILE REFERENCE: NeuroSearch 19313-001
; CURRENT APPLICATION NUMBER: US/09/347,613C
; CURRENT FILING DATE: 1999-07-02
; PRIOR APPLICATION NUMBER: DANISH 1998 00904
; PRIOR FILING DATE: 1998-07-06
; PRIOR APPLICATION NUMBER: USSN 60/092,229
; PRIOR FILING DATE: 1998-07-09
; PRIOR APPLICATION NUMBER: DANISH 1998 01048
; PRIOR FILING DATE: 1998-08-19
; PRIOR APPLICATION NUMBER: USSN 60/097,774
; PRIOR FILING DATE: 1998-08-25
; PRIOR APPLICATION NUMBER: DANISH 1998 01260
; PRIOR FILING DATE: 1998-10-05
; PRIOR APPLICATION NUMBER: USSN 60/103,908
; PRIOR FILING DATE: 1998-10-13
; PRIOR APPLICATION NUMBER: DANISH 1998 01265
; PRIOR FILING DATE: 1998-10-06
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 13
; LENGTH: 102
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-347-613C-13

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Best Local Similarity 61.0%; Pred. No. 2.4e+03;
Matches 36; Conservative 0; Mismatches 23; Indels 0; Gaps 0;

QY 149 GGCACAGAGCTCGCAGTCGGGCGAGGAGGGGGGAGAGAGAGCGGCTCTGGGCCC 207
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Db 74 GGCACAGGGCTGGCTGACGGGCGGAGGCCCGGGGGCGGTCCGACGGGCCCCGGGCCC 16

RESULT 11
US-09-662-183A-13/c
; Sequence 13, Application US/09662183A
; Patent No. 6734284
; GENERAL INFORMATION:
; APPLICANT: Johansen, Teit E.
; APPLICANT: Blom, Nikolaj
; APPLICANT: Hansen, Claus
; TITLE OF INVENTION: No. 6734284el Neurotrophic Factors
; FILE REFERENCE: 19313-001 DIV
; CURRENT APPLICATION NUMBER: US/09/662,183A
; CURRENT FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: DANISH 1998 00904
; PRIOR FILING DATE: 1998-07-06
; PRIOR APPLICATION NUMBER: USSN 60/092,229
; PRIOR FILING DATE: 1998-07-09
; PRIOR APPLICATION NUMBER: DANISH 1998 01048
; PRIOR FILING DATE: 1998-08-19
; PRIOR APPLICATION NUMBER: USSN 60/097,774
; PRIOR FILING DATE: 1998-08-25
; PRIOR APPLICATION NUMBER: DANISH 1998 01260
; PRIOR FILING DATE: 1998-10-05
; PRIOR APPLICATION NUMBER: USSN 60/103,908
; PRIOR FILING DATE: 1998-10-13
; PRIOR APPLICATION NUMBER: DANISH 1998 01265
; PRIOR FILING DATE: 1998-10-06
; PRIOR APPLICATION NUMBER: 09/347,613
; PRIOR FILING DATE: 2000-07-02
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 13
; LENGTH: 102
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-347-613C-13

Query Match      8.8%; Score 22.2; DB 3; Length 102;
Best Local Similarity 61.0%; Pred. No. 2.4e+03;
Matches 36; Conservative 0; Mismatches 23; Indels 0; Gaps 0;

QY 149 GGCACAGAGCTCGCAGTCGGGCGAGGAGGGGGGAGAGAGAGCGGCTCTGGGCCC 207
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 74 GGCACAGGGCTGGCTGACGGGCGGAGGCCCGGGGGCGGTCCGACGGGCCCCGGGCCC 16

RESULT 12
US-09-367-927A-1/c
; Sequence 1, Application US/09367927A
; Patent No. 6300126
; GENERAL INFORMATION:
; APPLICANT: GRUMMT, INGRID
; APPLICANT: RAINWEG, MITTLERER
; APPLICANT: GRUMMT, FRIEDERICK
; APPLICANT: VAN DER VOGELWEIDE STRASSE, WALTHER
; TITLE OF INVENTION: EXPRESSION VECTOR FOR THE PERMANENT
; TITLE OF INVENTION: EXPRESSION OF FOREIGN DNA
; FILE REFERENCE: 35280043US00
; CURRENT APPLICATION NUMBER: US/09/367,927A
; CURRENT FILING DATE: 1999-10-20
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 113
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-367-927A-1

Query Match      8.8%; Score 22.2; DB 3; Length 113;
Best Local Similarity 64.7%; Pred. No. 2.4e+03;
Matches 33; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

QY 147 GAGGCGACAGCTCGCAGTCGGGCGAGGAGGGGGGAGAGAGAGCGG 197
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RESULT 13
US-09-513-999C-20278/c
; Sequence 20278, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; Patent No. 6783961
; FILE REFERENCE: 59.US2.REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 20278
; LENGTH: 115
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-513-999C-20278

Query Match      8.8%; Score 22.2; DB 3; Length 115;
Best Local Similarity 61.0%; Pred. No. 2.4e+03;
Matches 36; Conservative 0; Mismatches 23; Indels 0; Gaps 0;

QY 169 GGCAGGAGGGGGGAGAGAGAGCGGCTCTGGCCCCCTTAATTGTACTTCGGGCTCG 227
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Db 63 GGCTGGGGCCCGGAGAGACAGCACCTCGAGCCAGAAATTGTTTCGCTTTCG 5

RESULT 14

US-07-964-624D-57/c
; Sequence 57, Application US/07964624D
; Patent No. 5496938
; GENERAL INFORMATION:
; APPLICANT: GOLD, LARRY M.
; APPLICANT: TURK, CRAIG
; TITLE OF INVENTION: METHOD OF SELECTING NUCLEIC
; TITLE OF INVENTION: ACIDS ON THE BASIS OF
; TITLE OF INVENTION: STRUCTURE
; NUMBER OF SEQUENCES: 83
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Swanson & Bratschun, L.L.C.
; CITY: Englewood
; STATE: Colorado
; COUNTRY: USA
; ZIP: 80111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3 1/5 inch, 1.44 MB
; COMPUTER: IBM compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/964,624D
; FILING DATE: 21-OCTOBER-1992
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/714,131
; FILING DATE: 10-JUNE-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/536,428
; FILING DATE: 11-JUNE-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Barry J. Swanson
; REGISTRATION NUMBER: 33,215
; REFERENCE/DOCKET NUMBER: NEX05
; TELEPHONE: (303) 793-3333
; TELEFAX: (303) 793-3333
; INFORMATION FOR SEQ ID NO: 57:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 86 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-07-964-624D-57

Query Match 8.7%; Score 21.8; DB 2; Length 86;
Best Local Similarity 56.2%; Pred. No. 3e+03;
Matches 41; Conservative 0; Mismatches 32; Indels 0; Gaps 0;

QY 84 CTCTGACTCCCTCGCACGGGCTGAGTTTCGGGCTCCAGGTTCCGGGTGTCGCCCTTGAGG 143
Db 86 CCGGATCCTCTTTACCTCTGTGTGAGCTCCAGAGTCCACTATCGTGTGTTCTCGATGGAG 27
QY 144 TTTGAGGCCAGAC 156
Db 26 TTGTCGGAAGGC 14

RESULT 15

US-08-442-062-57/c
; Sequence 57, Application US/08442062
; Patent No. 5595877
; GENERAL INFORMATION:
; APPLICANT: GOLD, LARRY M.
; APPLICANT: TURK, CRAIG
; TITLE OF INVENTION: METHOD OF SELECTING NUCLEIC
; TITLE OF INVENTION: ACIDS ON THE BASIS OF

; TITLE OF INVENTION: STRUCTURE
; NUMBER OF SEQUENCES: 83
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Swanson & Bratschun, L.L.C.
; STREET: 8400 E. Prentice Avenue, Suite 200
; CITY: Englewood
; STATE: Colorado
; COUNTRY: USA
; ZIP: 80111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3 1/5 inch, 1.44 MB
; COMPUTER: IBM compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/442,062
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/964,624
; FILING DATE: 21-OCTOBER-1992
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/714,131
; FILING DATE: 10-JUNE-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/536,428
; FILING DATE: 11-JUNE-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Barry J. Swanson
; REGISTRATION NUMBER: 33,215
; REFERENCE/DOCKET NUMBER: NEX05/D1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (303) 793-3333
; TELEFAX: (303) 793-3433
; INFORMATION FOR SEQ ID NO: 57:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 86 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-442-062-57

Query Match 8.7%; Score 21.8; DB 2; Length 86;
Best Local Similarity 56.2%; Pred. No. 3e+03;
Matches 41; Conservative 0; Mismatches 32; Indels 0; Gaps 0;

QY 84 CTCTGACTCCCTCGCACGGGCTGAGTTTCGGGCTCCAGGTTCCGGGTGTCGCCCTTGAGG 143
Db 86 CCGGATCCTCTTTACCTCTGTGTGAGCTCCAGAGTCCACTATCGTGTGTTCTCGATGGAG 27
QY 144 TTTGAGGCCAGAC 156
Db 26 TTGTCGGAAGGC 14

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GenCore version 5.1.9

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OM nucleic - nucleic search, using sw model

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- 12: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10G_PUBCOMB.seq:*
- 13: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11A_PUBCOMB.seq:*
- 14: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11B_PUBCOMB.seq:*
- 15: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11C_PUBCOMB.seq:*
- 16: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11D_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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C 2	25.2	10.0	96	16	US-11-173-902-22
C 3	25.2	10.0	109	9	US-10-674-124A-16551
C 4	24.6	9.8	103	9	US-10-357-930-3158
C 5	24.6	9.8	104	9	US-10-357-930-12327
C 6	24.2	9.6	105	6	US-10-106-698-3252
C 7	24	9.5	93	11	US-10-310-914A-17067
C 8	23.8	9.4	78	3	US-09-877-705A-145
C 9	23.8	9.4	78	3	US-09-947-274-145
C 10	23.8	9.4	78	3	US-09-877-738A-145
C 11	23.8	9.4	78	4	US-09-877-403A-145
C 12	23.8	9.4	78	4	US-10-779-595-145
C 13	23.4	9.3	100	10	US-10-781-499-1
C 14	23.4	9.3	120	3	US-09-796-692-6323
C 15	23.4	9.3	120	6	US-10-040-862-6323
C 16	23.4	9.3	120	7	US-10-057-475B-6323
C 17	23.4	9.3	120	7	US-10-154-884B-6323

18	23.4	9.3	120	9	US-10-764-324-6323	Sequence 6323, Ap
C 19	23.2	9.2	101	3	US-09-864-761-27544	Sequence 27544, A
C 20	23.2	9.2	118	7	US-10-029-386-21226	Sequence 21226, A
C 21	23	9.1	65	3	US-09-908-975-792	Sequence 792, App
C 22	23	9.1	87	3	US-09-294-093B-4883	Sequence 4883, Ap
C 23	22.8	9.0	60	3	US-09-908-975-16455	Sequence 16455, A
C 24	22.6	9.0	66	3	US-09-866-108-15685	Sequence 15685, A
C 25	22.6	9.0	66	8	US-10-723-361-15685	Sequence 15685, A
C 26	22.2	8.9	116	9	US-10-425-115-142012	Sequence 142012, A
C 27	22.2	8.9	102	3	US-09-804-615-13	Sequence 13, Appl
C 28	22.2	8.8	102	8	US-10-661-984A-13	Sequence 13, Appl
C 29	22.2	8.8	102	9	US-10-806-793-13	Sequence 13, Appl
C 30	22	8.7	68	10	US-10-490-955-387	Sequence 387, App
C 31	22	8.7	68	11	US-10-310-914A-2865	Sequence 2865, Ap
C 32	22	8.7	68	11	US-10-310-914A-3692	Sequence 3692, Ap
C 33	22	8.7	89	10	US-10-909-125-1425	Sequence 1425, Ap
C 34	22	8.7	99	11	US-10-310-914A-817	Sequence 817, App
C 35	22	8.7	104	8	US-10-242-535A-9222	Sequence 9222, Ap
C 36	22	8.7	104	8	US-10-085-783A-9222	Sequence 9222, Ap
C 37	22	8.7	113	3	US-09-864-761-21889	Sequence 21889, A
C 38	22	8.7	116	11	US-10-310-914A-12025	Sequence 12025, A
C 39	21.8	8.7	63	11	US-10-310-914A-20336	Sequence 20336, A
C 40	21.8	8.7	86	6	US-10-040-497-57	Sequence 57, Appl
C 41	21.8	8.7	86	9	US-10-818-954-57	Sequence 57, Appl
C 42	21.8	8.7	96	3	US-09-918-063-32	Sequence 32, Appl
C 43	21.8	8.7	96	3	US-09-918-063-34	Sequence 34, Appl
C 44	21.8	8.7	111	3	US-09-864-761-23937	Sequence 23937, A
C 45	21.8	8.7	113	3	US-09-933-797-725	Sequence 725, App

ALIGNMENTS

RESULT 1

US-10-310-914A-16611/c
 ; Sequence 16611, Application US/10310914A
 ; Publication No. US20060003322A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Bentwich, Isaac
 ; APPLICANT: Shiller, Kuvzat
 ; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
 ; TITLE OF INVENTION: uses thereof
 ; FILE REFERENCE: 06087.0200.CPUS01
 ; CURRENT APPLICATION NUMBER: US/10/310,914A
 ; CURRENT FILING DATE: 2002-12-06
 ; NUMBER OF SEQ ID NOS: 1388402
 ; SOFTWARE: PatentIn version 3.3
 ; SEQ ID NO 16611
 ; LENGTH: 67
 ; TYPE: RNA
 ; ORGANISM: Human
 ; US-10-310-914A-16611

Query Match 10.7%; Score 27; DB 11; Length 67;
 Best Local Similarity 85.7%; Pred. No. 2e+02; 5; Indels 0; Gaps 0;
 Matches 30; Conservative 0; Mismatches 5;

QY 174 GGAGGCGGGGAGAGACGAGCGGCTCTGCCCCCT 208
 |||||

DB 67 GGAGGCTGGGAGAGAGAGCCCTGCCCCCT 33
 |||||

RESULT 2

US-11-173-902-22/c
 ; Sequence 22, Application US/11173902
 ; Publication No. US20060057611A1
 ; GENERAL INFORMATION:
 ; APPLICANT: KAO, H. PIN
 ; APPLICANT: LAO, KAI QIN
 ; APPLICANT: JONES, ROBERT
 ; TITLE OF INVENTION: LOG-LINEAR AMPLIFICATION
 ; FILE REFERENCE: 375461-021US
 ; CURRENT APPLICATION NUMBER: US/11/173,902

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; CURRENT FILING DATE: 2005-06-30
; PRIOR APPLICATION NUMBER: 60/584,565
; PRIOR FILING DATE: 2004-06-30
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 22
; LENGTH: 96
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-11-173-902-22
;
Query Match 10.0%; Score 25.2; DB 16; Length 96;
Best Local Similarity 60.0%; Pred. No. 7.9e+02;
Matches 42; Conservative 0; Mismatches 28; Indels 0; Gaps 0;
QY 69 TCTGGATGCGAGTCCCTCTCACTCCCTCTGCCAGGCGCTGAGTTTCGGCTCCAGGTTCG 128
DB 90 TCCAGCTCCGACCCCTGTGAGACCTCAGCAACCTCTGTATTTTCGTGCACGGGTTC 31
QY 129 CGTGTGCCCC 138
DB 30 CGCTTGCCCC 21
RESULT 3
US-10-674-124A-16551
; Sequence 16551, Application US/10674124A
; Publication No. US20040197797A1
; GENERAL INFORMATION:
; APPLICANT: INOKO, Hidetoshi
; APPLICANT: TAMAYA, Gen
; TITLE OF INVENTION: GENE MAPPING METHOD USING MICROSATELLITE
; TITLE OF INVENTION: GENETIC POLYMORPHISM MARKERS
; FILE REFERENCE: ORIN-003CIP
; CURRENT APPLICATION NUMBER: US/10/674,124A
; CURRENT FILING DATE: 2003-09-26
; PRIOR APPLICATION NUMBER: 10/257,511
; PRIOR FILING DATE: 2003-03-07
; PRIOR APPLICATION NUMBER: PCT/JP00/07621
; PRIOR FILING DATE: 2000-10-30
; PRIOR APPLICATION NUMBER: JP2000-112699
; PRIOR FILING DATE: 2000-04-13
; PRIOR APPLICATION NUMBER: JP2002-327516
; PRIOR FILING DATE: 2002-09-28
; PRIOR APPLICATION NUMBER: JP2002-383869
; PRIOR FILING DATE: 2002-12-09
; NUMBER OF SEQ ID NOS: 27110
; SEQ ID NO 16551
; LENGTH: 109
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: DISD22_0010457
; FEATURE:
; OTHER INFORMATION: Located on chromosome 10
; FEATURE:
; OTHER INFORMATION: Distance between a terminus base of telomere on
; OTHER INFORMATION: chromosome short arm and 5'-terminus of this base
; OTHER INFORMATION: sequence : 92268095
; FEATURE:
; OTHER INFORMATION: Distance between 3'-terminus of neighbour sequence of
; OTHER INFORMATION: sequence listing upward to telomere on chromosomal short arm and
; OTHER INFORMATION: 5'-terminus of this base sequence : 79419
US-10-674-124A-16551
Query Match 10.0%; Score 25.2; DB 9; Length 109;
Best Local Similarity 62.9%; Pred. No. 7.9e+02;
Matches 39; Conservative 0; Mismatches 23; Indels 0; Gaps 0;
QY 138 CTGAGGTTTCAGGCCAGACAGCTCGCAGTCGGCAGGGCGGGGAGAGACGAGCGG 197
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DB 42 CTGAGTTTTCAGGCGGAGCAGGCGAGGCTAGCTGGACAGAGATACAGCAC 101
QY 198 CT 199
DB 102 CT 103
RESULT 4
US-10-357-930-3158
; Sequence 3158, Application US/10357930
; Publication No. US20040259086A1
; GENERAL INFORMATION:
; APPLICANT: Schlegel, Robert
; APPLICANT: Endege, Wilson
; APPLICANT: Monahan, John
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF
; TITLE OF INVENTION: HUMAN PROSTATE CANCER
; FILE REFERENCE: MRI-007BCN
; CURRENT APPLICATION NUMBER: US/10/357,930
; CURRENT FILING DATE: 2003-02-04
; PRIOR APPLICATION NUMBER: 09/785,276
; PRIOR FILING DATE: 2003-02-16
; PRIOR APPLICATION NUMBER: 60/183,319
; PRIOR FILING DATE: 2000-02-17
; PRIOR APPLICATION NUMBER: 60/189,862
; PRIOR FILING DATE: 2000-03-16
; PRIOR APPLICATION NUMBER: 60/207,454
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: 60/211,314
; PRIOR FILING DATE: 2000-06-09
; PRIOR APPLICATION NUMBER: 60/219,007
; PRIOR FILING DATE: 2000-07-18
; PRIOR APPLICATION NUMBER: 60/255,281
; NUMBER OF SEQ ID NOS: 62232
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3158
; LENGTH: 103
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-357-930-3158
Query Match 9.8%; Score 24.6; DB 9; Length 103;
Best Local Similarity 57.0%; Pred. No. 1.2e+03;
Matches 45; Conservative 0; Mismatches 34; Indels 0; Gaps 0;
QY 174 GGAGGGCGGGGAGAGACGAGCGGCTCTGGCCCCCTTAATTGTACTTCGGGCTCGTATTGT 233
DB 2 GGTACGGGGGAGACGCCGCCGCGCTGCGAGCGCTGTAGTCGCTTCGTCGTTT 61
QY 234 CTCTCCTTTCCGCACTCC 252
DB 62 CTCTTCCTTCGCTAACGCC 80
RESULT 5
US-10-357-930-12327
; Sequence 12327, Application US/10357930
; Publication No. US20040259086A1
; GENERAL INFORMATION:
; APPLICANT: Schlegel, Robert
; APPLICANT: Endege, Wilson
; APPLICANT: Monahan, John
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF
; TITLE OF INVENTION: HUMAN PROSTATE CANCER
; FILE REFERENCE: MRI-007BCN
; CURRENT APPLICATION NUMBER: US/10/357,930
; CURRENT FILING DATE: 2003-02-04
; PRIOR APPLICATION NUMBER: 09/785,276
; PRIOR FILING DATE: 2003-02-16
```

PRIOR APPLICATION NUMBER: 60/193,319
PRIOR FILING DATE: 2000-02-17
PRIOR APPLICATION NUMBER: 60/189,862
PRIOR FILING DATE: 2000-03-16
PRIOR APPLICATION NUMBER: 60/207,454
PRIOR FILING DATE: 2000-05-25
PRIOR APPLICATION NUMBER: 60/211,314
PRIOR FILING DATE: 2000-06-09
PRIOR APPLICATION NUMBER: 60/219,007
PRIOR FILING DATE: 2000-07-18
PRIOR APPLICATION NUMBER: 60/255,281
PRIOR FILING DATE: 2000-12-13
NUMBER OF SEQ ID NOS: 62232
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 12327
LENGTH: 104
TYPE: DNA
ORGANISM: Homo sapiens
US-10-357-930-12327

Query Match 9.8%; Score 24.6; DB 9; Length 104;
Best Local Similarity 57.0%; Pred. No. 1.2e+03;
Matches 45; Conservative 0; Mismatches 34; Indels 0; Gaps 0;

QY 174 GGAGGGGGGGAGACGACGCGCTCTGCCCCCTTAATTGTACTTCGGGCTCGTATTGT 233
DB 2 GGTACGGGGGAGACGCGCGCGCTGCGACGCTGTAGTGGCTTCGTCTCGGTTTTT 61

QY 234 CTCTCCTTTCCGCCACCTCC 252
DB 62 CTCTCCTTCGCTAACGCC 80

RESULT 6
US-10-106-698-3252
Sequence 3252, Application US/10106698
Publication No. US20030109690A1
GENERAL INFORMATION:
APPLICANT: Ruben et al.
TITLE OF INVENTION: Colon and Colon Cancer Associated Polynucleotides and Polypeptide
FILE REFERENCE: PA005P1
CURRENT APPLICATION NUMBER: US/10/106,698
CURRENT FILING DATE: 2002-03-27
PRIOR APPLICATION NUMBER: PCT/US00/26524
PRIOR FILING DATE: 2000-09-28
PRIOR APPLICATION NUMBER: US 60/157,137
PRIOR FILING DATE: 1999-09-29
PRIOR APPLICATION NUMBER: US 60/163,280
PRIOR FILING DATE: 1999-11-03
NUMBER OF SEQ ID NOS: 8564
SOFTWARE: PatentIn Ver. 3.0
SEQ ID NO 3252
LENGTH: 105
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
LOCATION: (28)..(28)
OTHER INFORMATION: n equals a.t.g, or c
NAME/KEY: misc feature
LOCATION: (40)..(40)
OTHER INFORMATION: n equals a.t.g, or c
NAME/KEY: misc feature
LOCATION: (53)..(53)
OTHER INFORMATION: n equals a.t.g, or c
NAME/KEY: misc feature
LOCATION: (72)..(72)
OTHER INFORMATION: n equals a.t.g, or c
NAME/KEY: misc feature
LOCATION: (77)..(77)
OTHER INFORMATION: n equals a.t.g, or c
US-10-106-698-3252

Query Match 9.6%; Score 24.2; DB 6; Length 105;
Best Local Similarity 53.7%; Pred. No. 1.6e+03;
Matches 44; Conservative 0; Mismatches 38; Indels 0; Gaps 0;

QY 96 CTGCCACGGGCTGAGTTTCGGCTCCAGGTTCCGGTGTGCGCTGAGGTTTGAGGCGCAGA 155
DB 24 CCGCNACGCCCGCAGGNACGGTCCGGAANTCCGGGTGACCCACGCTTCNGCCAAA 83

QY 156 CAGCTCGCAGTCGGGCGAGGAG 177
DB 84 CATGGCGGGCAGGACGGGGG 105

RESULT 7
US-10-310-914A-17067
Sequence 17067, Application US/10310914A
Publication No. US20060003322A1
GENERAL INFORMATION:
APPLICANT: Bentwich, Isaac
APPLICANT: Shiller, Kvuzat
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
TITLE OF INVENTION: uses thereof
FILE REFERENCE: 06087.0200.CPUS01
CURRENT APPLICATION NUMBER: US/10/310,914A
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: PatentIn version 3.3
SEQ ID NO 17067
LENGTH: 93
TYPE: RNA
ORGANISM: Human
US-10-310-914A-17067

Query Match 9.5%; Score 24; DB 11; Length 93;
Best Local Similarity 51.8%; Pred. No. 1.9e+03;
Matches 29; Conservative 7; Mismatches 20; Indels 0; Gaps 0;

QY 126 TCGGTGTGCGCTGAGTTTGAGCCAGCAGCTGCGGCGAGGGGCG 181
DB 38 UCGGUUUCACCCGUGUUUUGCGGAGAGGCGUGUCCCGUGCGGGGGCG 93

RESULT 8
US-09-877-705A-145/c
Sequence 145, Application US/09877705A
Publication No. US20030008283A1
GENERAL INFORMATION:
APPLICANT: Li, Jason
TITLE OF INVENTION: METHOD FOR SCREENING FOR DRUG CANDIDATES FOR MODULATING TRANSCRIPT
TITLE OF INVENTION: FACTOR ACTIVITY
FILE REFERENCE: 26757-704
CURRENT APPLICATION NUMBER: US/09/877,705A
CURRENT FILING DATE: 2001-08-16
NUMBER OF SEQ ID NOS: 162
SOFTWARE: PatentIn version 3.1
SEQ ID NO 145
LENGTH: 78
TYPE: DNA
ORGANISM: Artificial sequence
FEATURE:
OTHER INFORMATION: Hybridization probe MP74
US-09-877-705A-145

Query Match 9.4%; Score 23.8; DB 3; Length 78;
Best Local Similarity 59.7%; Pred. No. 2.1e+03;
Matches 40; Conservative 0; Mismatches 27; Indels 0; Gaps 0;

QY 109 AGTTTCCGGCTCCAGGTTCCGGTGTGCGCTGAGGTTTGAGCCAGCAGCTGCGAGTCG 168
DB 78 AGCTTCAGGTCAGAGGTCAGAGAGTAGCTTCAGGTCAGAGGTCAGAGGTCAGGTCAG 19
QY 169 GGCAGGG 175

Db 18 GTCAGAG 12

RESULT 9

US-09-947-274-145/c
; Sequence 145, Application US/09947274
; Publication No. US20030017499A1
; GENERAL INFORMATION:
; APPLICANT: Li, Xianqiang

; TITLE OF INVENTION: METHOD FOR DETECTING TRANSCRIPTION FACTOR-PROTEIN INTERACTIONS

; FILE REFERENCE: 26757-705
; CURRENT APPLICATION NUMBER: US/09/947,274
; CURRENT FILING DATE: 2001-09-05
; PRIOR APPLICATION NUMBER: US 09/877,738
; PRIOR FILING DATE: 2000-06-08
; PRIOR APPLICATION NUMBER: US 09/877,243
; PRIOR FILING DATE: 2000-06-08
; PRIOR APPLICATION NUMBER: US 09/877,403
; PRIOR FILING DATE: 2000-06-08
; PRIOR APPLICATION NUMBER: US 09/877,705
; PRIOR FILING DATE: 2000-06-08

; NUMBER OF SEQ ID NOS: 162
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 145

; LENGTH: 78

; TYPE: DNA

; ORGANISM: Artificial sequence

; FEATURE:

; OTHER INFORMATION: Hybridization probe MP74

US-09-947-274-145

Query Match

Best Local Similarity 9.4%; Score 23.8; DB 3; Length 78;

Matches 40; Conservative 0; Mismatches 27; Indels 0; Gaps 0;

QY 109 AGTTTCGGCTCCAGGTTCCGCTGTCGCCCTGAGGTTTGAGGCCAGACAGCTCGCAGTCG 168

Db 78 AGCTTCAGGTCAGAGGTCAGAGAGCTAGCTTTCAGGTCAGAGGTCAGAGAGCTAGCTTTCAG 19

QY 169 GGCAGGG 175

Db 18 GTCAGAG 12

RESULT 10

US-09-877-738A-145/c
; Sequence 145, Application US/0987738A
; Publication No. US20030022173A1
; GENERAL INFORMATION:
; APPLICANT: Li, Jason

; TITLE OF INVENTION: METHOD AND KIT FOR ISOLATING DNA PROBES THAT BIND TO ACTIVATED

; FILE REFERENCE: 26757-701

; CURRENT APPLICATION NUMBER: US/09/877,738A

; CURRENT FILING DATE: 2001-06-01

; NUMBER OF SEQ ID NOS: 162

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 145

; LENGTH: 78

; TYPE: DNA

; ORGANISM: Artificial sequence

; FEATURE:

; OTHER INFORMATION: Hybridization probe MP74

US-09-877-738A-145

Query Match

Best Local Similarity 9.4%; Score 23.8; DB 3; Length 78;

Matches 40; Conservative 0; Mismatches 27; Indels 0; Gaps 0;

QY 109 AGTTTCGGCTCCAGGTTCCGCTGTCGCCCTGAGGTTTGAGGCCAGACAGCTCGCAGTCG 168

Db 78 AGCTTCAGGTCAGAGGTCAGAGAGCTAGCTTTCAGGTCAGAGGTCAGAGAGCTAGCTTTCAG 19

QY 169 GGCAGGG 175

Db 18 GTCAGAG 12

RESULT 11

US-09-877-403A-145/c
; Sequence 145, Application US/09877403A
; Publication No. US20040214166A1
; GENERAL INFORMATION:
; APPLICANT: Li, Jason

; TITLE OF INVENTION: METHOD FOR IDENTIFYING A DISEASE STATE BASED ON A DETECTED MIXTURE

; FILE REFERENCE: 26757-703

; CURRENT APPLICATION NUMBER: US/09/877,403A

; CURRENT FILING DATE: 2001-08-10

; NUMBER OF SEQ ID NOS: 162

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 145

; LENGTH: 78

; TYPE: DNA

; ORGANISM: Artificial sequence

; FEATURE:

; OTHER INFORMATION: Hybridization probe MP74

US-09-877-403A-145

Query Match

Best Local Similarity 9.4%; Score 23.8; DB 4; Length 78;

Matches 40; Conservative 0; Mismatches 27; Indels 0; Gaps 0;

QY 109 AGTTTCGGCTCCAGGTTCCGCTGTCGCCCTGAGGTTTGAGGCCAGACAGCTCGCAGTCG 168

Db 78 AGCTTCAGGTCAGAGGTCAGAGAGCTAGCTTTCAGGTCAGAGGTCAGAGAGCTAGCTTTCAG 19

QY 169 GGCAGGG 175

Db 18 GTCAGAG 12

RESULT 12

US-10-779-595-145/c
; Sequence 145, Application US/10779595
; Publication No. US20040132090A1
; GENERAL INFORMATION:
; APPLICANT: Li, Xianqiang

; TITLE OF INVENTION: METHOD, ARRAY AND KIT FOR DETECTING ACTIVATED TRANSCRIPTION FACTOR

; FILE REFERENCE: 26757-702.301

; CURRENT APPLICATION NUMBER: US/10/779,595

; CURRENT FILING DATE: 2004-02-13

; PRIOR APPLICATION NUMBER: 09/877,243

; PRIOR FILING DATE: 2001-06-08

; NUMBER OF SEQ ID NOS: 162

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 145

; LENGTH: 78

; TYPE: DNA

; ORGANISM: Artificial sequence

; FEATURE:

; OTHER INFORMATION: Hybridization probe MP74

US-10-779-595-145

Query Match

Best Local Similarity 9.4%; Score 23.8; DB 8; Length 78;

Matches 40; Conservative 0; Mismatches 27; Indels 0; Gaps 0;

QY 109 AGTTTCGGCTCCAGGTTCCGCTGTCGCCCTGAGGTTTGAGGCCAGACAGCTCGCAGTCG 168

Db 78 AGCTTCAGGTCAGAGGTCAGAGAGCTAGCTTTCAGGTCAGAGGTCAGAGAGCTAGCTTTCAG 19

QY 169 GGCAGGG 175

Db 18 GTCAGAG 12

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RESULT 13
US-10-781-499-1
; Sequence 1, Application US/10781499
; Publication No. US20050054060A1
; GENERAL INFORMATION:
; APPLICANT: Metabolic Explorer
; TITLE OF INVENTION: Method for the preparation of an evolved microorganism for the ch
; TITLE OF INVENTION: or modification of metabolic pathways
; FILE REFERENCE: D20701/ 345774
; CURRENT APPLICATION NUMBER: US/10/781,499
; CURRENT FILING DATE: 2004-02-18
; PRIOR APPLICATION NUMBER: FR 0301924
; PRIOR FILING DATE: 2003-02-18
; PRIOR APPLICATION NUMBER: FR 0305768
; PRIOR FILING DATE: 2003-05-14
; PRIOR APPLICATION NUMBER: FR 0305769
; PRIOR FILING DATE: 2003-05-14
; PRIOR APPLICATION NUMBER: FR 0313054
; PRIOR FILING DATE: 2003-11-06
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 100
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: DmetER
US-10-781-499-1

Query Match          9.3%; Score 23.4; DB 10; Length 100;
Best Local Similarity 63.2%; Pred. No. 3e+03;
Matches 36; Conservative 0; Mismatches 21; Indels 0; Gaps 0;

QY 100 CAGCGCTGATTCGGCTCCAGGTCGCTCGCTCGCCCTGAGGTTTGAGGCCAGAC 156
DB 12 CAAGTTCTGCGCCCTGCACCATGTTCCGCAATGTCGCGCGCGGTTTCTGCGCCAGCC 68

RESULT 14
US-09-796-692-6323
; Sequence 6323, Application US/09796692
; Publication No. US20020198362A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Algate, Paul A.
; APPLICANT: Mannion, Jane
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DETECTION, DIAGNOSIS AND THERAPY
; FILE REFERENCE: 2077.001200
; CURRENT APPLICATION NUMBER: US/09/796,692
; CURRENT FILING DATE: 2001-03-01
; PRIOR APPLICATION NUMBER: 60/186,126
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: 60/190,479
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: 60/200,545
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: 60/200,303
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: 60/200,779
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: 60/200,999
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: 60/206,201
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: 60/218,950
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: 60/222,903
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: 60/223,416
; PRIOR FILING DATE: 2000-08-04
; PRIOR APPLICATION NUMBER: 60/223,378
; PRIOR FILING DATE: 2000-08-07
; PRIOR APPLICATION NUMBER: 60/200,999
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: 60/202,084
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: 60/206,201
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: 60/218,950
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: 60/222,903
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: 60/223,416
; PRIOR FILING DATE: 2000-08-04
; PRIOR APPLICATION NUMBER: 60/223,378
; PRIOR FILING DATE: 2000-08-07
; PRIOR APPLICATION NUMBER: 60/200,999
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: 60/202,084
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: 60/206,201
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: 60/218,950
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: 60/222,903
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: 60/223,416
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; PRIOR FILING DATE: 2000-08-04
; PRIOR APPLICATION NUMBER: 60/223,378
; PRIOR FILING DATE: 2000-08-07
; NUMBER OF SEQ ID NOS: 9597
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 6323
; LENGTH: 120
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-796-692-6323

Query Match          9.3%; Score 23.4; DB 3; Length 120;
Best Local Similarity 60.0%; Pred. No. 3e+03;
Matches 39; Conservative 0; Mismatches 26; Indels 0; Gaps 0;

QY 141 AGGTTTGAGGCCAGACAGCTCGCAGTCGCGGCGAGGAGCGCGGGGAGAGACGACGCGGCTC 200
DB 53 AGGTTTGATGCAAGATGCTCTGGGAAGTGCCAGCATATGGGGGAGAGAAAGCTGCTC 112

QY 201 TGGCC 205
DB 113 AGACC 117

RESULT 15
US-10-040-862-6323
; Sequence 6323, Application US/10040862
; Publication No. US20030078396A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Algate, Paul A.
; APPLICANT: Mannion, Jane
; APPLICANT: Retter, Marc
; APPLICANT: Corixa Corporation
; TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy
; FILE REFERENCE: 014058-013520US
; CURRENT APPLICATION NUMBER: US/10/040,862
; CURRENT FILING DATE: 2001-11-06
; PRIOR APPLICATION NUMBER: US 60/186,126
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: US 60/190,479
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: US 60/200,545
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 60/200,303
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,779
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,999
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: US 60/202,084
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: US 60/206,201
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: US 60/218,950
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 60/222,903
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: US 60/223,416
; PRIOR FILING DATE: 2000-08-04
; PRIOR APPLICATION NUMBER: US 60/223,378
; PRIOR FILING DATE: 2000-08-07
; PRIOR APPLICATION NUMBER: US 09/796,692
; PRIOR FILING DATE: 2001-03-01
; NUMBER OF SEQ ID NOS: 10467
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 6323
; LENGTH: 120
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-040-862-6323
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GenCore version 5.1.9
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OM nucleic - nucleic search, using sw model

Run on: October 16, 2006, 13:43:59 ; Search time 1855 Seconds
(without alignments)
253.830 Million cell updates/sec

Title: US-10-604-726A-8797
Perfect score: 252
Sequence: 1 ggggtatctgcaactgagag.....tctctctttgcccacctcc 252

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 2395520 seqs, 934235491 residues

Total number of hits satisfying chosen parameters: 3233144

Minimum DB seq length: 0
Maximum DB seq length: 120

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications NA_New:
1: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09_NEW_PUB.seq.*
2: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US06_NEW_PUB.seq.*
3: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US07_NEW_PUB.seq.*
4: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US08_NEW_PUB.seq.*
5: /EMC_Celerra_SIDS3/ptodata/2/pubpna/PCT_NEW_PUB.seq.*
6: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10_NEW_PUB.seq.*
7: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11_NEW_PUB.seq.*
8: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11_NEW_PUB.seq.*
9: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11_NEW_PUB.seq.*
10: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US60_NEW_PUB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	22	8.7	102	7	US-11-043-824-258
C 2	21.2	8.4	98	9	US-11-365-556-82
C 3	21	8.3	47	7	US-11-370-584-3264
C 4	21	8.3	103	8	US-11-266-748A-424752
C 5	20.8	8.3	106	8	US-11-266-748A-307408
C 6	20.6	8.2	47	7	US-11-370-584-2971
C 7	20.6	8.2	100	6	US-10-874-990B-90
C 8	20.6	8.2	112	8	US-11-266-748A-300647
C 9	20.4	8.1	68	8	US-11-194-055-199
C 10	20.4	8.1	86	8	US-11-194-055-198
C 11	20.4	8.1	86	8	US-11-194-055-277
C 12	20	7.9	80	8	US-11-169-140-46
C 13	20	7.9	80	8	US-11-191-244-63
C 14	20	7.9	95	8	US-11-169-140-47
C 15	20	7.9	95	8	US-11-191-244-64
C 16	20	7.9	115	9	US-11-348-413-10828
C 17	19.8	7.9	76	7	US-11-222-346A-42
C 18	19.8	7.9	110	8	US-11-266-748A-419451
C 19	19.6	7.8	98	9	US-11-365-556-80
C 20	19.6	7.8	98	9	US-11-365-556-81
C 21	19.6	7.8	98	9	US-11-365-556-83
C 22	19.4	7.7	47	7	US-11-370-584-995
C 23	19.4	7.7	102	7	US-11-244-330A-888

24	19.2	7.6	89	7	US-11-356-568A-42	Sequence 42, Appl
C 25	19.2	7.6	107	8	US-11-266-748A-411535	Sequence 411535,
C 26	19.2	7.6	117	7	US-11-244-330A-6708	Sequence 6708, Ap
C 27	19	7.5	61	8	US-11-296-931-1	Sequence 1, Appli
C 28	19	7.5	118	7	US-11-314-834-4644	Sequence 4644, Ap
C 29	18.8	7.5	114	7	US-11-043-842-279	Sequence 279, App
C 30	18.6	7.4	99	8	US-11-217-529-173876	Sequence 173876,
C 31	18.6	7.4	106	8	US-11-266-748A-420020	Sequence 420020,
C 32	18.6	7.4	108	8	US-11-266-748A-232793	Sequence 232793,
C 33	18.4	7.3	47	7	US-11-370-584-612	Sequence 612, App
C 34	18.4	7.3	51	8	US-11-143-642-1090	Sequence 1090, Ap
C 35	18.4	7.3	75	9	US-11-348-413-1748	Sequence 1748, Ap
C 36	18.4	7.3	77	6	US-10-834-268-4016	Sequence 4016, Ap
C 37	18.4	7.3	81	7	US-11-292-078-9878	Sequence 9878, Ap
C 38	18.4	7.3	103	8	US-11-266-748A-413307	Sequence 413307,
C 39	18.4	7.3	109	7	US-11-244-330A-3545	Sequence 3545, Ap
C 40	18.4	7.3	113	9	US-11-348-413-9862	Sequence 9862, Ap
C 41	18.2	7.2	50	6	US-10-554-711-648	Sequence 648, App
C 42	18.2	7.2	50	6	US-10-554-759-648	Sequence 648, App
C 43	18.2	7.2	60	8	US-11-069-910-46	Sequence 46, Appl
C 44	18.2	7.2	99	6	US-10-531-545-10	Sequence 10, Appl
C 45	18.2	7.2	117	7	US-11-320-072-15	Sequence 15, Appl

ALIGNMENTS

RESULT 1

US-11-043-824-258/c
; Sequence 258, Application US/11043824
; Publication No. US20060172311A1
; GENERAL INFORMATION:
; APPLICANT: Compugen Ltd
; TITLE OF INVENTION: NOVEL NUCLEOTIDE AND AMINO ACID SEQUENCES, AND ASSAYS AND METHODS
; TITLE OF INVENTION: THEREOF FOR DIAGNOSIS OF CARDIAC DISEASE
; FILE REFERENCE: 1847,1007
; CURRENT APPLICATION NUMBER: US/11/043,824
; CURRENT FILING DATE: 2005-01-27
; NUMBER OF SEQ ID NOS: 452
; SEQ ID NO 258
; LENGTH: 102
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide
US-11-043-824-258

Query Match 8.7%; Score 22; DB 7; Length 102;
Best Local Similarity 53.5%; Pred. No. 3.8e+03;
Matches 46; Conservative 0; Mismatches 40; Indels 0; Gaps 0;

QY	44	TTGGAAGGGCGCTTTCCTCTCTGATGTCAGAGTCTCTGACTCCCTCTGCCAGC 103
Db	86	TTGAGGGAGCGTTGGGCTCTTCTAGCTTCACGGGTACTCATTTGGCTGCTCCAGC 27
QY	104	GGCTGAGTTTCGGGTCCTCCAGGTTCCG 129
Db	26	GTCCGAGACATTTCTCCAGGTTTGC 1

RESULT 2

US-11-365-556-82
; Sequence 82, Application US/11365556
; Publication No. US2006016252A1
; GENERAL INFORMATION:
; APPLICANT: LADNER, ROBERT C.
; APPLICANT: COHEN, EDWARD H.
; APPLICANT: NASTRI, HORACIO G.
; APPLICANT: ROOKEY, KRISTIN L.
; APPLICANT: HOET, RENE
; TITLE OF INVENTION: NOVEL METHODS OF CONSTRUCTING LIBRARIES OF GENETIC
; TITLE OF INVENTION: PACKAGES THAT COLLECTIVELY DISPLAY THE MEMBERS OF A
; TITLE OF INVENTION: DIVERSE FAMILY OF PEPTIDES, POLYPEPTIDES OR PROTEINS

```
; FILE REFERENCE: DVAX/002
; CURRENT APPLICATION NUMBER: US/11/365,556
; CURRENT FILING DATE: 2006-02-28
; PRIOR APPLICATION NUMBER: US/09/837,306
; PRIOR FILING DATE: 2001-04-17
; PRIOR APPLICATION NUMBER: 60/198,069
; PRIOR FILING DATE: 2000-04-17
; NUMBER OF SEQ ID NOS: 428
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 82
; LENGTH: 98
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-365-556-82

Query Match      8.4%; Score 21.2; DB 9; Length 98;
Best Local Similarity 60.3%; Pred. No. 6.Se+03;
Matches 35; Conservative 0; Mismatches 23; Indels 0; Gaps 0;

Qy 66 TTTTCTGGATGCAGTCTCTGACTCCCTCTGCCAGGGCTGAGTTTCGGGCTCCAG 123
Db 38 TCCTCCTGAAGCTGAGCTGTGACTGCCGACACAGCGCCGTGTATTACTGTGGCCAG 95

RESULT 3
US-11-370-584-3264/c
; Sequence 3264, Application US/11370584
; Publication No. US20060177863A1
; GENERAL INFORMATION:
; APPLICANT: Cohen, Daniel
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Chumakov, Ilya
; TITLE OF INVENTION: Biallelic markers for use in constructing a high
; FILE REFERENCE: GENSET.020CP1
; CURRENT APPLICATION NUMBER: US/11/370,584
; CURRENT FILING DATE: 2006-03-08
; PRIOR APPLICATION NUMBER: US/10/349,143
; PRIOR FILING DATE: 2003-01-21
; PRIOR APPLICATION NUMBER: US/09/422,978
; PRIOR FILING DATE: 1999-10-20
; PRIOR APPLICATION NUMBER: US 09/298,850
; PRIOR FILING DATE: 1999-04-21
; PRIOR APPLICATION NUMBER: US 60/109,732
; PRIOR FILING DATE: 1998-11-23
; PRIOR APPLICATION NUMBER: US 60/082,614
; PRIOR FILING DATE: 1998-04-21
; NUMBER OF SEQ ID NOS: 11796
; SEQ ID NO 3264
; LENGTH: 47
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: allele
; LOCATION: 24
; OTHER INFORMATION: 99-2832-152 : polymorphic base C or T
US-11-370-584-3264

Query Match      8.3%; Score 21; DB 7; Length 47;
Best Local Similarity 91.3%; Pred. No. 5.8e+03;
Matches 21; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 170 GCAGGAGGGCGGGGAGAGACG 192
Db 42 GCAGGAGGGCGGAGGAGRACG 20

RESULT 4
US-11-266-748A-424752/c
; Sequence 424752, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
```

```
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcriptome Microarray Technology and
; TITLE OF INVENTION: Methods of Using the Same
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266,748A
; CURRENT FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 424752
; LENGTH: 103
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-266-748A-424752

Query Match      8.3%; Score 21; DB 8; Length 103;
Best Local Similarity 66.7%; Pred. No. 7.5e+03;
Matches 30; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

Qy 69 TCTGGATGCAGTCTCTGACTCCCTCTGCCAGGGCTGAGTTT 113
Db 63 TCTTGGTGGCGAGAACTGTGTTCTGTCGCCCCGCTGCATTT 19

RESULT 5
US-11-266-748A-307408
; Sequence 307408, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcriptome Microarray Technology and
; TITLE OF INVENTION: Methods of Using the Same
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266,748A
; CURRENT FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 307408
; LENGTH: 106
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```
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-266-748A-307408

Query Match      8.3%; Score 20.8; DB 8; Length 106;
Best Local Similarity 55.6%; Pred. No. 8.7e+03;
Matches 40; Conservative 0; Mismatches 32; Indels 0; Gaps 0;

QY 59 GCTTCTGTTTCTGGATGAGAGTCTCTGACTCCCTCTGCCACGGGCTGAGTTTCCGGC 118
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 15 GCTTGACTGTACAGCATGTTGTTTCTATGCTCTCTGGGCTCAGGCGCTTCATGTTCCGGT 74
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 119 TCCAGGTTCCGG 130
    ||||| ||||| |||||
Db 75 GACTGATTACCG 86
    ||||| ||||| |||||

RESULT 6
US-11-370-584-2971
; Sequence 2971, Application US/11370584
; Publication No. US20060177863A1
; GENERAL INFORMATION:
; APPLICANT: Cohen, Daniel
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Chumakov, Ilya
; TITLE OF INVENTION: Biallelic markers for use in constructing a high
; FILE REFERENCE: GENSET.020CP1
; CURRENT APPLICATION NUMBER: US/11/370,584
; CURRENT FILING DATE: 2006-03-08
; PRIOR APPLICATION NUMBER: US/10/349,143
; PRIOR FILING DATE: 2003-01-21
; PRIOR APPLICATION NUMBER: US/09/422,978
; PRIOR FILING DATE: 1999-10-20
; PRIOR APPLICATION NUMBER: US 09/298,850
; PRIOR FILING DATE: 1999-04-21
; PRIOR APPLICATION NUMBER: US 60/109,732
; PRIOR FILING DATE: 1998-11-23
; PRIOR APPLICATION NUMBER: US 60/082,614
; PRIOR FILING DATE: 1998-04-21
; NUMBER OF SEQ ID NOS: 11796
; SEQ ID NO 2971
; LENGTH: 47
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: allele
; LOCATION: 24
; OTHER INFORMATION: 99-21310-416 : polymorphic base A or G
US-11-370-584-2971

Query Match      8.2%; Score 20.6; DB 7; Length 47;
Best Local Similarity 70.3%; Pred. No. 7.7e+03;
Matches 26; Conservative 1; Mismatches 10; Indels 0; Gaps 0;

QY 55 CTTTGCTTCTGTTTCTGGATGAGAGTCTCTGACT 91
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 5 CTTGATGCTCTTCTCTCTCTCCAGATCTCTGGCT 41
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 7
US-10-874-990B-90
; Sequence 90, Application US/10874990B
; Publication No. US20060216303A1
; GENERAL INFORMATION:
; APPLICANT: SOMANTA LIMITED
; APPLICANT: do COUTO, Fernando J.R.
; APPLICANT: CERIANI, Roberto L.
; APPLICANT: PETERSON, Jerry A.
; APPLICANT: PADLAN, Eduardo A.
; TITLE OF INVENTION: PROCESSES AND PRODUCTS WITH MODIFIED ANTIBODIES OF HUMAN MILK FAT
; FILE REFERENCE: SOMA1140-4
```

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; CURRENT APPLICATION NUMBER: US/10/874,990B
; CURRENT FILING DATE: 2004-06-23
; PRIOR APPLICATION NUMBER: US 09/947,839
; PRIOR FILING DATE: 2001-09-06
; PRIOR APPLICATION NUMBER: US 08/976,288
; PRIOR FILING DATE: 1997-11-21
; PRIOR APPLICATION NUMBER: US 08/129,930
; PRIOR FILING DATE: 1993-09-30
; PRIOR APPLICATION NUMBER: US 07/977,696
; PRIOR FILING DATE: 1992-11-12
; NUMBER OF SEQ ID NOS: 125
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 90
; LENGTH: 100
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Primer
US-10-874-990B-90

Query Match      8.2%; Score 20.6; DB 6; Length 100;
Best Local Similarity 59.3%; Pred. No. 9.8e+03;
Matches 35; Conservative 0; Mismatches 24; Indels 0; Gaps 0;

QY 64 TCTTTTCTGGATGAGAGTCTCTGACTCCCTCTGCCACGGGCTGAGTTTCCGGCTCCA 122
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 33 TGTGTTGATGACCCAACTCTCTCTCCCTGTCTCCTCAGGAGAGCCAGCCCTCCA 91
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 8
US-11-266-748A-300647/c
; Sequence 300647, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcriptome Microarray Technology and
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266,748A
; CURRENT FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 300647
; LENGTH: 112
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-266-748A-300647

Query Match      8.2%; Score 20.6; DB 8; Length 112;
Best Local Similarity 59.3%; Pred. No. 1e+04;
Matches 35; Conservative 0; Mismatches 24; Indels 0; Gaps 0;

QY 128 GGTGTGTCGCCCTTGGAGTTTGGAGCCAGAGTCCGAGTCGGGCGAGGAGGGGGGGA 186
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 75 GTGTGAGTATGGAGGGGCCAAGCCAGACAGCTGCACGCCGATGGGCGAGGTGGGGCA 17
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
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```
RESULT 9
US-11-194-055-199
; Sequence 199, Application US/11194055
; Publication No. US20060105360A1
; GENERAL INFORMATION:
; APPLICANT: Croce, Carlo M.
; APPLICANT: Liu, Chang-Gong
; APPLICANT: Calin, George, A.
; APPLICANT: Cinzia, Sevignani
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF CANCERS WITH
; TITLE OF INVENTION: MICRORNA LOCATED IN OR NEAR CANCER-ASSOCIATED CHROMOSOMAL
; TITLE OF INVENTION: FEATURES
; FILE REFERENCE: 3589.1018-008
; CURRENT APPLICATION NUMBER: US/11/194,055
; CURRENT FILING DATE: 2005-07-29
; PRIOR APPLICATION NUMBER: PCT/US2005/004865
; PRIOR FILING DATE: 2005-02-09
; PRIOR APPLICATION NUMBER: 60/543,119
; PRIOR FILING DATE: 2004-02-09
; PRIOR APPLICATION NUMBER: 60/542,929
; PRIOR FILING DATE: 2004-02-09
; PRIOR APPLICATION NUMBER: 60/542,963
; PRIOR FILING DATE: 2004-02-09
; PRIOR APPLICATION NUMBER: 60/542,940
; PRIOR FILING DATE: 2004-02-09
; PRIOR APPLICATION NUMBER: 60/580,959
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 60/580,797
; PRIOR FILING DATE: 2004-06-18
; NUMBER OF SEQ ID NOS: 663
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 199
; LENGTH: 68
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-194-055-199

Query Match      8.1%; Score 20.4; DB 8; Length 68;
Best Local Similarity 61.1%; Pred. No. 9.9e+03;
Matches 33; Conservative 0; Mismatches 21; Indels 0; Gaps 0;

QY      64  TGTTCCTGATGCAGAGTCCTCTGACTCCCTCTGCCACGGGTGAGTTTCGGG 117
Db      13  TGCATGGTGAGGGTGAGCTTCTGAAAACCCCTCCCATCATGCAGGGTTTGAG 66

RESULT 10
US-11-194-055-198
; Sequence 198, Application US/11194055
; Publication No. US20060105360A1
; GENERAL INFORMATION:
; APPLICANT: Croce, Carlo M.
; APPLICANT: Liu, Chang-Gong
; APPLICANT: Calin, George, A.
; APPLICANT: Cinzia, Sevignani
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF CANCERS WITH
; TITLE OF INVENTION: MICRORNA LOCATED IN OR NEAR CANCER-ASSOCIATED CHROMOSOMAL
; TITLE OF INVENTION: FEATURES
; FILE REFERENCE: 3589.1018-008
; CURRENT APPLICATION NUMBER: US/11/194,055
; CURRENT FILING DATE: 2005-07-29
; PRIOR APPLICATION NUMBER: PCT/US2005/004865
; PRIOR FILING DATE: 2005-02-09
; PRIOR APPLICATION NUMBER: 60/543,119
; PRIOR FILING DATE: 2004-02-09
; PRIOR APPLICATION NUMBER: 60/542,929
; PRIOR FILING DATE: 2004-02-09
; PRIOR APPLICATION NUMBER: 60/542,963
; PRIOR FILING DATE: 2004-02-09
; PRIOR APPLICATION NUMBER: 60/580,959
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 60/580,797
; PRIOR FILING DATE: 2004-06-18
; NUMBER OF SEQ ID NOS: 663
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 199
; LENGTH: 68
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-194-055-199

Query Match      8.1%; Score 20.4; DB 8; Length 68;
Best Local Similarity 61.1%; Pred. No. 9.9e+03;
Matches 33; Conservative 0; Mismatches 21; Indels 0; Gaps 0;

QY      64  TGTTCCTGATGCAGAGTCCTCTGACTCCCTCTGCCACGGGTGAGTTTCGGG 117
Db      13  TGCATGGTGAGGGTGAGCTTCTGAAAACCCCTCCCATCATGCAGGGTTTGAG 66

RESULT 11
US-11-194-055-277
; Sequence 277, Application US/11194055
; Publication No. US20060105360A1
; GENERAL INFORMATION:
; APPLICANT: Croce, Carlo M.
; APPLICANT: Liu, Chang-Gong
; APPLICANT: Calin, George, A.
; APPLICANT: Cinzia, Sevignani
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF CANCERS WITH
; TITLE OF INVENTION: MICRORNA LOCATED IN OR NEAR CANCER-ASSOCIATED CHROMOSOMAL
; TITLE OF INVENTION: FEATURES
; FILE REFERENCE: 3589.1018-008
; CURRENT APPLICATION NUMBER: US/11/194,055
; CURRENT FILING DATE: 2005-07-29
; PRIOR APPLICATION NUMBER: PCT/US2005/004865
; PRIOR FILING DATE: 2005-02-09
; PRIOR APPLICATION NUMBER: 60/543,119
; PRIOR FILING DATE: 2004-02-09
; PRIOR APPLICATION NUMBER: 60/542,929
; PRIOR FILING DATE: 2004-02-09
; PRIOR APPLICATION NUMBER: 60/542,963
; PRIOR FILING DATE: 2004-02-09
; PRIOR APPLICATION NUMBER: 60/542,940
; PRIOR FILING DATE: 2004-02-09
; PRIOR APPLICATION NUMBER: 60/580,959
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 60/580,797
; PRIOR FILING DATE: 2004-06-18
; NUMBER OF SEQ ID NOS: 663
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 277
; LENGTH: 86
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-194-055-277

Query Match      8.1%; Score 20.4; DB 8; Length 86;
Best Local Similarity 61.1%; Pred. No. 1.1e+04;
Matches 33; Conservative 0; Mismatches 21; Indels 0; Gaps 0;

QY      64  TGTTCCTGATGCAGAGTCCTCTGACTCCCTCTGCCACGGGTGAGTTTCGGG 117
Db      22  TGCATGGTGAGGGTGAGCTTCTGAAAACCCCTCCCATCATGCAGGGTTTGAG 75

RESULT 12
US-11-169-140-46/c
; Sequence 46, Application US/11169140
; Publication No. US20060099150A1
; GENERAL INFORMATION:
; APPLICANT: ARIZEKE PHARMACEUTICALS, INC.
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; PRIOR APPLICATION NUMBER: 60/580,959
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 60/580,797
; PRIOR FILING DATE: 2004-06-18
; NUMBER OF SEQ ID NOS: 663
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 198
; LENGTH: 86
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-194-055-198
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Query Match      8.1%; Score 20.4; DB 8; Length 86;
Best Local Similarity 61.1%; Pred. No. 1.1e+04;
Matches 33; Conservative 0; Mismatches 21; Indels 0; Gaps 0;

QY      64  TGTTCCTGATGCAGAGTCCTCTGACTCCCTCTGCCACGGGTGAGTTTCGGG 117
Db      22  TGCATGGTGAGGGTGAGCTTCTGAAAACCCCTCCCATCATGCAGGGTTTGAG 75
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RESULT 11
US-11-194-055-277
; Sequence 277, Application US/11194055
; Publication No. US20060105360A1
; GENERAL INFORMATION:
; APPLICANT: Croce, Carlo M.
; APPLICANT: Liu, Chang-Gong
; APPLICANT: Calin, George, A.
; APPLICANT: Cinzia, Sevignani
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF CANCERS WITH
; TITLE OF INVENTION: MICRORNA LOCATED IN OR NEAR CANCER-ASSOCIATED CHROMOSOMAL
; TITLE OF INVENTION: FEATURES
; FILE REFERENCE: 3589.1018-008
; CURRENT APPLICATION NUMBER: US/11/194,055
; CURRENT FILING DATE: 2005-07-29
; PRIOR APPLICATION NUMBER: PCT/US2005/004865
; PRIOR FILING DATE: 2005-02-09
; PRIOR APPLICATION NUMBER: 60/543,119
; PRIOR FILING DATE: 2004-02-09
; PRIOR APPLICATION NUMBER: 60/542,929
; PRIOR FILING DATE: 2004-02-09
; PRIOR APPLICATION NUMBER: 60/542,963
; PRIOR FILING DATE: 2004-02-09
; PRIOR APPLICATION NUMBER: 60/542,940
; PRIOR FILING DATE: 2004-02-09
; PRIOR APPLICATION NUMBER: 60/580,959
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 60/580,797
; PRIOR FILING DATE: 2004-06-18
; NUMBER OF SEQ ID NOS: 663
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 277
; LENGTH: 86
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-194-055-277
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Query Match      8.1%; Score 20.4; DB 8; Length 86;
Best Local Similarity 61.1%; Pred. No. 1.1e+04;
Matches 33; Conservative 0; Mismatches 21; Indels 0; Gaps 0;

QY      64  TGTTCCTGATGCAGAGTCCTCTGACTCCCTCTGCCACGGGTGAGTTTCGGG 117
Db      22  TGCATGGTGAGGGTGAGCTTCTGAAAACCCCTCCCATCATGCAGGGTTTGAG 75

RESULT 12
US-11-169-140-46/c
; Sequence 46, Application US/11169140
; Publication No. US20060099150A1
; GENERAL INFORMATION:
; APPLICANT: ARIZEKE PHARMACEUTICALS, INC.
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Search completed: October 16, 2006, 14:41:52
Job time : 1856 secs
